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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:42:39 ; Search time 59 Seconds
(without alignments)
1896.421 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLALEQTKDPQGEDGQNNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	396	6	ABG70700 Human ser
2	2104	100.0	396	6	ABU62276 Human kin
3	2089	99.3	396	4	AAB85491 Human pro
4	2089	99.3	396	5	AAE14261 Novel hum
5	2089	99.3	396	5	AAE21725 Human PKI
6	2083	99.0	396	5	AAM50334 Human 149
7	2047	97.3	407	5	AAE14260 Human hum
8	1500.5	71.3	327	4	AAU03504 Human pro
9	1427	67.8	404	6	ABU62277 Mouse ser
10	1425.5	67.8	403	6	ABU62278 Human ser
11	1425.5	67.8	414	4	AAB65600 Novel pro
12	1425.5	67.8	414	5	ABP43807 Serine/th
13	1425.5	67.8	414	5	AAO17710 Human ser
14	1425.5	67.8	414	6	ABR58617 Human can
15	1425.5	67.8	414	7	ADE38375 Human pro
16	1325	63.0	419	4	AAB65599 Novel pro
17	1321	62.8	425	4	AAM40592 Human pol
18	1318	62.6	485	5	AAE24141 Human kin
19	1317.5	62.6	384	6	ABU62279 Mouse ser
20	1317.5	62.6	488	5	AAO17709 Murine se
21	1315	62.5	419	4	AAM38806 Human pol
22	1302	61.9	488	6	ABO14992 Human NOV
23	1285.5	61.1	713	5	ABB06090 Human NS
24	1278.5	60.8	399	5	ABB84300 Murine se
25	1259.5	59.9	375	4	AAE04371 Human kin

26	1201.5	57.1	364	4	AAU29309	Aau29309 Human PRO
27	1201.5	57.1	364	6	ABU58685	Abu58685 Human PRO
28	1201.5	57.1	364	6	ABU88233	Abu88233 Novel hum
29	1201.5	57.1	364	6	ABU84548	Abu84548 Human sec
30	1201.5	57.1	364	6	ABR66422	ABr66422 Human sec
31	1201.5	57.1	364	6	ABR65812	ABr65812 Human sec
32	1201.5	57.1	364	6	ABU99752	Abu99752 Human sec
33	1201.5	57.1	364	6	ABU82991	Abu82991 Human PRO
34	1201.5	57.1	364	6	ABU90112	Abu90112 Novel hum
35	1201.5	57.1	364	6	ABR68361	ABr68361 Human hum
36	1201.5	57.1	364	6	ABU96414	Abu96414 Novel hum
37	1201.5	57.1	364	6	ABU92845	Abu92845 Human sec
38	1201.5	57.1	364	6	ABO08922	ABo08922 Human sec
39	1201.5	57.1	364	6	ABO02974	ABo02974 Human sec
40	1201.5	57.1	364	6	ABR75128	ABr75128 Human sec
41	1201.5	57.1	364	6	ABR94890	ABr94890 Human sec
42	1201.5	57.1	364	6	ABU85863	Abu85863 Human PRO
43	1201.5	57.1	364	6	ABU99023	Abu99023 Novel hum
44	1201.5	57.1	364	6	ABU98238	Abu98238 Novel hum
45	1201.5	57.1	364	6	ABU91944	Abu91944 Novel hum

ALIGNMENTS

RESULT 1
ABG70700
ID ABG70700 standard; protein; 396 AA.
XX
AC ABG70700;
XX
DT 17-JAN-2003 (first entry)
XX
DE Human serine/threonine protein kinase-like kinase.
XX
KW Human; kinase; serine/threonine kinase; immune response; transgenic;
KW enzyme.
XX
OS Homo sapiens.

Key	Location/Qualifiers
Modified-site	2..7
Modified-site	/label= N_myristoylation_site
Modified-site	4..7
Modified-site	/label= N_glycosylation_site
Modified-site	5..7
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Modified-site	6..8
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Binding-site	29..52
Binding-site	/label= Protein_kinase_ATP-binding_region
Modified-site	33..36
Modified-site	/label= Casein_kinase_II_phosphorylation_site
Modified-site	43..46
Modified-site	/label= N_glycosylation_site
Modified-site	45..47
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Modified-site	89..92
Modified-site	/label= Casein_kinase_II_phosphorylation_site
Modified-site	122..124
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Active-site	142..154
Active-site	/label= Serine/threonine_protein_kinase_active_site
Modified-site	193..195
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Modified-site	194..196
Modified-site	/label= Protein_kinase_C_phosphorylation_site
Modified-site	197..202
Modified-site	/label= N_myristoylation_site
Modified-site	212..215
Modified-site	/label= Casein_kinase_II_phosphorylation_site
Modified-site	218..221
Modified-site	/label= Amidation_site

FT Modified-site 230..233
FT /label= Casein_kinase_II_phosphorylation_site
FT Modified-site 391..396
FT /label= N_myristoylation_site
XX US2002127683-A1.
PN
XX
PD 12-SEP-2002.
XX
XX 09-MAR-2001; 2001US-00801876.
PF
XX
PR 09-MAR-2001; 2001US-00801876.
XX
XX (YEJ/J) YE J.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
XX
PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2003-028938/02.
DR N-PSDB; ABS55499, ABS55500.
XX

Novel isolated human kinase peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the kinase protein, and as immunogens to raise antibodies.

Claim 1; Fig 2; 174pp; English.

The present invention relates to the isolation of a human kinase and the polynucleotide sequences encoding it. The human kinase of the invention is related to the serine/threonine kinase subfamily. The gene encoding the human kinase is located on chromosome 5. The polypeptide and polynucleotide sequences of the invention are useful for treating a disease or condition mediated by a human kinase. Both the polypeptide and polynucleotide sequences are useful as models for the development of human therapeutics, for identifying therapeutic proteins, as targets for development of human therapeutic agents, and as query sequences to perform a search against sequence data bases to identify other family members of related sequences. The polypeptide is useful to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed, in drug screening assays, in cell-based or cell-free systems, to identify compounds that modulate kinase activity of the protein in its natural state, or an altered form that causes the specific disease or pathology associated with the kinase, to screen a compound for the ability to stimulate or inhibit interaction between the kinase protein and a molecule that normally interacts with the kinase protein, and in pharmacogenomic analysis. The polynucleotide is useful for monitoring the effectiveness of modulating compounds on the expression or activity of the human kinase gene in clinical trials or in a treatment regimen, in diagnostic assays for qualitative changes in a human kinase nucleic acid that leads to a pathology, for testing an individual for a genotype that while not necessarily causing a disease, nevertheless affects the treatment modality, as antisense constructs to control human kinase gene expression in cells, tissues and organisms, for gene therapy in patients containing cells that are aberrant in human kinase gene expression, and to produce transgenic animals. The present sequence represents a human kinase related to the serine/threonine protein kinase subfamily

SQ Sequence 396 AA;

Query Match 100.0%; Score 2104; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.1e-194;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKQCAMKYMNRKQCV 60
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKQCAMKYMNRKQCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMDLYLQNRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPHYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPHYHRSSTSSKEIVHTPET 240
QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPMNDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPMNDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKCKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKCKDMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNRFNKRQPNLALQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNRFNKRQPNLALQTKDPQGEDGQNNNL 396

RESULT 2

ABU62276

ID ABU62276 standard; protein; 396 AA.

XX AC ABU62276;

DT 01-SEP-2003 (first entry)

XX Human kinase.

XX Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis; arteriosclerosis.

OS Homo sapiens.

XX US2003027307-A1.

PD 06-FEB-2003.

XX 26-SEP-2002; 2002US-00254869.

XX 09-MAR-2001; 2001US-00801876.

XX (APPL-) APPLERA CORP.

PI Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-492035/58.

DR N-PSDB; ACA62840, ACA62841.

XX New isolated human kinase proteins, useful for treating disorders mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis or psoriasis), or for development of human therapeutics and diagnostic compositions.

PS Claim 1; Fig 2A; 185pp; English.

XX The invention relates to a new isolated human kinase peptide. The human kinase peptide and nucleic acid molecules are useful in the development of human therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. cancers, inflammations, arteriosclerosis or psoriasis) characterised by an absence of, inappropriate, or unwanted expression of the kinase protein. These molecules are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The peptides are also useful for raising antibodies or eliciting an immune response; as a reagent (including the labelled reagent) in assays

CC designed to quantitatively determine levels of the protein (or its
CC binding partner or ligand) in biological fluids; or as markers for
CC tissues in which the corresponding protein is preferentially expressed.
CC The agents identified are useful for treating a subject with a disorder
CC mediated by kinase pathway. The present sequence represents the amino
CC acid sequence of a human kinase
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 2104; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.1e-194;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKQKCV 60
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFK 120
DB 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFK 120

QY 121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180
DB 121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180

QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSSTSSKEIVHTFET 240
DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSSTSSKEIVHTFET 240

QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGPIP 300
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGPIP 300

QY 301 NKGRNLCDPTFELEEMILESKPLHKKQRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
DB 301 NKGRNLCDPTFELEEMILESKPLHKKQRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
DB 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 3
AAB85491
ID AAB85491 standard; protein; 396 AA.

AC AAB85491;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase SGK177.
XX
KW Protein kinase; enzyme; cytosolic; neurotrophic; neuroprotective; human;
KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
KW antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic;
KW osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;
KW vasotropic; antidiabetic; gene therapy.
OS Homo sapiens.
XX
PN WO200155356-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002337.
XX
PR 25-JAN-2000; 2000US-0178078P.
PR 31-JAN-2000; 2000US-0179364P.
PR 17-FEB-2000; 2000US-0183173P.
PR 17-MAR-2000; 2000US-0190162P.
PR 29-MAR-2000; 2000US-0193404P.
PR 13-NOV-2000; 2000US-0247013P.

XX (SUGE-) SUGEN INC.
XX
PI Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR WPI; 2001-476202/51.
XX N-PSDB; AAB46891.
XX
PT Kinase polypeptides useful for treating cancers, Alzheimer's disease,
PT viral infections, diabetes, obesity, organ transplant rejection and
PT rheumatoid arthritis.
XX
PS Claim 7; Page 214; 218pp; English.

XX The invention provides human protein kinases and protein kinase-like
CC enzymes and polynucleotides encoding the polypeptides. The kinase
CC polypeptides and their modulators are useful for treating a disease or
CC disorder such as cancer, immune-related diseases, cardiovascular disease,
CC brain or neuronal-associated disease and metabolic disorders, including
CC cancers of tissues, cancers of hematopoietic origin, diseases of the
CC central nervous system, diseases of the peripheral nervous system,
CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
CC lateral sclerosis, viral infections, infections caused by prions,
CC bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
CC mood disorders, attention disorders, cognitive disorders, hypotension,
CC hypertension, psychotic disorders, neurological disorders, dyskinesias,
CC metabolic disorders, and organ transplant rejection. They are also useful
CC for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
CC osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
CC inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
CC such as diabetes, obesity, cardiovascular diseases such as reperfusion
CC injury, coronary thrombosis, clotting disorders and atherosclerosis,
CC ocular diseases such as glaucoma, retinopathy and macular degeneration,
CC psychiatric and neurological disorders such as anxiety, schizophrenia,
CC dementia, manic depression, etc. The polynucleotides are useful in gene
CC therapy techniques to treat the above mentioned disorders. Sequences
CC AAB85491-85522 represent the human protein kinases of the invention

XX Sequence 396 AA;

Query Match 99.3%; Score 2089; DB 4; Length 396;
Best Local Similarity 99.5%; Pred. No. 2.3e-192;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKQKCV 60
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFK 120
DB 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFK 120

QY 121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180
DB 121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180

QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSSTSSKEIVHTFET 240
DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSSTSSKEIVHTFET 240

QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGPIP 300
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGPIP 300

QY 301 NKGRNLCDPTFELEEMILESKPLHKKQRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
DB 301 NKGRNLCDPTFELEEMILESKPLHKKQRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
DB 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 4
AAE14261
ID AAE14261 standard; protein; 396 AA.
XX
AC AAE14261;
XX
DT 07-MAR-2002 (first entry)
XX
DE Novel human protein (NHP) kinase #4.
XX
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic.
XX
OS Homo sapiens.
XX
PN WO200181557-A2.
XX
PD 01-NOV-2001.
XX
PF 24-APR-2001; 2001WO-US013149.
XX
PR 25-APR-2000; 2000US-0199499P.
PR 01-MAY-2000; 2000US-0201227P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
XX
DR WPI; 2002-034442/04.
DR N-PSDB; AAD23679.
XX
PT New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.
XX
PS Claim 7; Page 43; 44pp; English.
XX
CC The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-
CC dependent kinases related to the invention
SQ Sequence 396 AA;

Query Match 99.3%; Score 2089; DB 5; Length 396;
Best Local Similarity 99.5%; Pred. No. 2.3e-192;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKMKAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKMKAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLLGDDLRYHLQNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLLGDDLRYHLQNVHFK 120

Qy 121 ETVKLFCELVMAALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
Db 121 ETVKLFCELVMAALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPEMFSSRRKGAGYSFAVDWWSLGVATAYELLGRRPYHIRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRRKGAGYSFAVDWWSLGVATAYELLGRRPYHIRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFIP 300

Qy 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKKCKMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKKCKMRKCDSSQTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNRFNKRQPNLALBQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNRFNKRQPNLALBQTKDPQGEDGQNNNL 396

RESULT 5
AAE21725
ID AAE21725 standard; protein; 396 AA.
XX
AC AAE21725;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human PKIN-20 protein.
XX
KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia;
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;
KW Down's syndrome; gene therapy; protein therapy; cytostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 13..300 /note= "Protein kinase domain"
FT Domain 23..300 /note= "Protein kinase domain"
FT Domain 23..281 /note= "Eukaryotic protein kinase domain"
FT Domain 25..270 /note= "Protein kinase domain"
FT Domain 25..268 /note= "Protein kinase domain"
XX WO200218557-A2.
PN 07-MAR-2002.
XX 31-AUG-2001; 2001WO-US027219.
PR 31-AUG-2000; 2000US-0229873P.
PR 08-SEP-2000; 2000US-0231357P.
PR 14-SEP-2000; 2000US-0232654P.
PR 22-SEP-2000; 2000US-0234902P.
PR 29-SEP-2000; 2000US-0236499P.
PR 06-OCT-2000; 2000US-0238389P.
PR 13-OCT-2000; 2000US-0240542P.
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Bandnan O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
PI Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
PI Burford N;
XX WPI; 2002-329769/36.
DR

CC a cellular proliferation and/or differentiation disorder, especially
CC lung, colon, brain and breast cancer, uses a small molecule, peptide,
CC phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.
CC Other disorders that may be diagnosed/treated include those associated
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,
CC liver disorders, viral diseases, pain and metabolic disorders
XX

SQ Sequence 396 AA;

Query Match 99.0%; Score 2083; DB 5; Length 396;

Best Local Similarity 99.2%; Pred. No. 8.6e-192;

Matches 393; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGKAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGKAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNNVHFK 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDENIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDENIAAMLPRETIQITM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAAYELLGRRPYHIRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAAYELLGRRPYHIRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQKRLIPGPI 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQKRLIPGPI 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCLLQHLDSVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCLLQHLDSVQKEFI 360
QY 361 IFNREKVNDRDNKRPQNLALAEQTKPQGEDGQNNL 396
Db 361 IFNREKVNDRDNKRPQNLALAEQTKPQGEDGQNNL 396

RESULT 7

AAE14260
ID AAE14260 standard; protein; 407 AA.

AC AAE14260;

DT 07-MAR-2002 (first entry)

DE Novel human protein (NHP) kinase #3.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic.

OS Homo sapiens.

PN WO200181557-A2.

PD 01-NOV-2001.

PF 24-APR-2001; 2001WO-US013149.

PR 25-APR-2000; 2000US-0199499P.

PR 01-MAY-2000; 2000US-0201227P.

PA (LEXI-) LEXICON GENETICS INC.

PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX WPI; 2002-034442/04.

DR N-PSDB; AAD23678.

XX

PT New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.

XX Claim 5; Page 41-42; 44pp; English.

XX

CC The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-
CC dependent kinases related to the invention

SQ Sequence 407 AA;

Query Match 97.3%; Score 2047; DB 5; Length 407;

Best Local Similarity 98.7%; Pred. No. 2.6e-188;

Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGKAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGKAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNNVHFK 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDENIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDENIAAMLPRETIQITM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAAYELLGRRPYHIRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAAYELLGRRPYHIRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQKRLIPGPI 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQKRLIPGPI 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCLLQHLDSVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCLLQHLDSVQKEFI 360
QY 361 IFNREKVNDRDNKRPQNLALAEQTKPQGEDGQ 392
Db 361 IFNREKVNDRDNKRPQNLALAEQTKPQVTNGQ 392

RESULT 8

AAU03504

ID AAU03504 standard; protein; 327 AA.

XX AAU03504;

AC AAU03504;

DT 12-SEP-2001 (first entry)

DE Human protein kinase #4.

XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW reproductiv disorder.
XX
OS Homo sapiens.
XX WO200138503-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US032085.
XX
XX 24-NOV-1999; 99US-0167482P.
XX
XX (SUGE-) SUGEN INC.
XX
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI: 2001-343950/36.
DR N-PSDB; AAS06704.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX
XX Claim 7; Fig 2; 433pp; English.
XX
XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 327 AA;

Query Match 71.3%; Score 1500.5; DB 4; Length 327;
Best Local Similarity 87.0%; Pred. No. 9.1e-136;
Matches 295; Conservative 6; Mismatches 19; Indels 19; Gaps 4;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKKMCAMKYNKQKCV 60
Db |||||
1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKKMCAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 120
Db |||||
61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db |||||
121 ETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRKGAGYSPAVDWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKGAGYSPAVDWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKKLLE---PNPDQRFSLSDVQ---NFPYMDINWDVAFQKR 293
Db |||||
241 TVVTYPSAWSQEMVSLKKVRRKTACPNEVTKGSRLSGLSLEVSIOY-----WGHQLSSL 295
QY 294 LIPGFI PNKGRNLCDPTFELEEMILES KPLHKKKKRLAK 332
Db |||||
296 -----QKGRNLCDPTFELEEMILES KPLHKKKKRLAK 327

RESULT 9
ABU62277
ID ABU62277 standard; protein; 404 AA.
XX
AC ABU62277;
XX
DT 01-SEP-2003 (first entry)
XX
DE Mouse serine/threonine protein kinase #1.
XX
KW Mouse; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;
KW arteriosclerosis.
XX
OS Mus musculus.
XX
PN US2003027307-A1.
XX
PD 06-FEB-2003.
XX
PF 26-SEP-2002; 2002US-00254869.
XX
PR 09-MAR-2001; 2001US-00801876.
XX
PA (APPL-) APPLERA CORP.
XX
PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2003-492035/58.
XX
XX New isolated human kinase proteins, useful for treating disorders
PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
PT or psoriasis), or for development of human therapeutics and diagnostic
PT compositions.
XX
PS Disclosure; Fig 2B; 185pp; English.
XX
XX The invention relates to a new isolated human kinase peptide. The human
CC kinase peptide and nucleic acid molecules are useful in the development
CC of human therapeutics and diagnostic compositions. The peptides are
CC useful for treating disorders (e.g. cancers, inflammations, arteriosclerosis or psoriasis) characterised by an absence of,
CC inappropriate, or unwanted expression of the kinase protein. These
CC molecules are particularly useful as models for developing human
CC therapeutic targets, identifying therapeutic proteins, or serving as
CC targets for the development of human therapeutic agents that modulate
CC kinase activity in cells and tissues that express the kinase. The
CC peptides are also useful for raising antibodies or eliciting an immune
CC response; as a reagent (including the labelled reagent) in assays
CC designed to quantitatively determine levels of the protein (or its
CC binding partner or ligand) in biological fluids; or as markers for
CC tissues in which the corresponding protein is preferentially expressed.
CC The agents identified are useful for treating a subject with a disorder
CC mediated by kinase pathway. The present sequence represents the amino
CC acid sequence of the mouse serine/threonine protein kinase #1
XX
SQ Sequence 404 AA;

Query Match 67.8%; Score 1427; DB 6; Length 404;
Best Local Similarity 69.5%; Pred. No. 1.5e-128;
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKKMCAMKYNKQKCV 60
Db |||||
1 MGGNHSKPPVFDENEENVDHFIQLRAIGKSGFGEVCIVQNDTKKMCAMKYNKQKCV 60
QY 61 -ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 119
Db |||||
61 QERDEVNRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMAVDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTT 179
Db |||||

Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAITVLKGEKASS 180
QY 180 MAGTKPYMAPEMFS--SRKGAGYSFAVDWMSLGVTAAYELLRGRPPYHIRSTSSKEIVHT 237
Db 181 MAGTKPYMAPEVFQVYDGGPGYSYPVDWMSLGVTAAYELLRGRPPYHIRSTSSKEIVHT 240
QY 238 PETTVVTPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINWDVAVFQKRLIPG 297
Db 241 FKVERVHYSSWCEGMSVLLKLLTKDPESRLSSLDIQSMYTLADWMDVAVFEKALMPG 300
QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356
Db 301 FVFNKGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRDSSTKDSCLNGLHQQCLETVR 360
QY 357 KEFIIIFNREKVRNDRFNKQPNLALEQTKDPQGEDGQNNNL 396
Db 361 KEFIIIFNREKLRQ-----QGHGQLSDL 384

RESULT 10
ABU62278
ID ABU62278 standard; protein; 403 AA.

XX AC ABU62278;
XX DT 01-SEP-2003 (first entry)
XX DE Human serine/threonine protein kinase #1.
XX KW Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;
XX KW arteriosclerosis.
XX OS Homo sapiens.
XX OS US2003027307-A1.
XX PD 06-FEB-2003.
XX PF 26-SEP-2002; 2002US-00254869.
XX PR 09-MAR-2001; 2001US-00801876.
XX PA (APPL-) APPLERA CORP.
XX PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX DR WPI; 2003-492035/58.
XX PT New isolated human kinase proteins, useful for treating disorders
PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
PT or psoriasis), or for development of human therapeutics and diagnostic
PT compositions.
XX PS Disclosure; Fig 2B; 185pp; English.
XX CC The invention relates to a new isolated human kinase peptide. The human
CC kinase peptide and nucleic acid molecules are useful in the development
CC of human therapeutics and diagnostic compositions. The peptides are
CC useful for treating disorders (e.g. cancers, inflammations,
CC arteriosclerosis or psoriasis) characterised by an absence of,
CC inappropriate, or unwanted expression of the kinase protein. These
CC molecules are particularly useful as models for developing human
CC therapeutic targets, identifying therapeutic proteins, or serving as
CC targets for the development of human therapeutic agents that modulate
CC kinase activity in cells and tissues that express the kinase. The
CC peptides are also useful for raising antibodies or eliciting an immune
CC response; as a reagent (including the labelled reagent) in assays
CC designed to quantitatively determine levels of the protein (or its
CC binding partner or ligand) in biological fluids; or as markers for
CC tissues in which the corresponding protein is preferentially expressed.
CC The agents identified are useful for treating a subject with a disorder
CC mediated by kinase pathway. The present sequence represents the amino
CC acid sequence of the human serine/threonine protein kinase #1

XX SQ Sequence 403 AA;
Query Match 67.8%; Score 1425.5; DB 6; Length 403;
Best Local Similarity 68.2%; Pred. No. 2.1e-128;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;
QY 1 MGANTSRRKPPVDFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKQCAMKMYNKQKCV 60
Db 1 MGGHSHKPPVDFDENEEVNFDFEILRAIGKSGFGEVCIVQKNDTKKQCAMKMYNKQKCI 60
QY 61 ERNEVRNVFKEIQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
Db 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVVKGAERASSM 180
QY 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWMSLGVTAAYELLRGRPPYHIRSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVFQVYDGGPGYSYPVDWMSLGVTAAYELLRGRPPYHIRSTSSKEIVHTF 240
QY 239 BTTVVTPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINWDVAVFQKRLIPGF 298
Db 241 KVERVHYSSWCEGMSVLLKLLTKDPESRVSSLDIQSVPYLADWMDVAVFEKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357
Db 301 VFNKGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRDSSTKDSCLNGLHQQCLETVRE 360
QY 358 BFIIFNREKVRNDRFNKQPNLALEQTKDPQ-----EDGQNNNL 396
Db 361 BFIIFNREKLRQ-----QGHGQLSDL 403

RESULT 11
AAB65600
ID AAB65600 standard; protein; 414 AA.
XX AC AAB65600;
XX DT 27-MAR-2001 (first entry)
XX DE Novel protein kinase, SEQ ID NO: 125.

XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX OS Homo sapiens.
XX PN WO200073469-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014842.
XX PR 28-MAY-1999; 99US-0136503P.
XX PA (SUGE-) SUGEN INC.
XX PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX DR WPI; 2001-032161/04.
XX DR N-PSDB; AAF44625.
XX PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.

RESULT 13
AAO17710
ID AAO17710 standard; protein; 414 AA.
XX
AC AAO17710;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human serine-threonine protein kinase #2.
XX
KW Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW central nervous system disorder; inflammation; gene therapy; COPD;
KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW antidiabetic; antiallergic; antiaesthmic; antidepressant; anorectic;
KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW enzyme.
XX
OS Homo sapiens.
XX
PN WO200233056-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-EP011892.
XX
PR 16-OCT-2000; 2000US-0240097P.
PR 30-JUL-2001; 2001US-0308096P.
XX
PA (FARB) BAYER AG.
XX
PI Koehler RH;
XX
DR WPI; 2002-435534/46.
XX
PT New human serine-threonine protein kinase and encoding polynucleotides,
PT useful for diagnosing, treating and preventing central nervous system
PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS Disclosure; Fig 8; 135pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC human serine-threonine protein kinase. The sequences can be used in the
CC diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC chronic obstructive pulmonary disease (COPD). The present sequence is a
CC human serine-threonine protein kinase
XX
SQ Sequence 414 AA;

Query Match 67.8%; Score 1425.5; DB 5; Length 414;
Best Local Similarity 68.2%; Pred. No. 2.2e-128;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGANTSRRKPPVDENEEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKWCAMKYMKNQKCV 60
Db 1 MGGNHSRKPVPFDENEEVNFDHFQILRAIGKSGFGKVCIVQKRDTKKWMYAMKYMKNQKCI 60

Qy 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFTTE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVVKGAERASM 180

Qy 181 AGTKPYMAPEMPS--SRKAGYSFAVDWWSLGTAYELLRGRPHYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVQVYMDRPGYSGYSPVDWWSLGTAYELLRGRPHYHRSVTPIDEILNMF 240

Qy 239 ETTVVTVTSAWSQEMVSLKLLLEPNPDRFQSLSDVQNFPPYMDINWDVAVFQKRLIPGF 298

Db 241 KVERVHYSTWCKGMVALLRKLTKDPESRVSSLHDIQSVPYLADNWDVAVFKKALMPGE 300
Qy 299 IPNKGRLNCDPTFEEEMILESKPLHKKKKRLAK-KKQMRKCDSSQTCLLQEHLDVQK 357
Db 301 VPKGRLNCDPTFEEEMILESKPLHKKKKRLAKRSDGTGKDCPLNGHLQHCLETVRE 360
Qy 358 EFIIFNREKVRNDRFNKRPNLALEQTKDPQG----EDGQNNNL 396
Db 361 EFIIFNREKLRQGGQSGQLLDTDSRGGGQAQSKLQDGCNNNL 403

RESULT 14
ABR58617
ID ABR58617 standard; protein; 414 AA.
XX
AC ABR58617;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:274.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72764.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 748; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these

CC pathologies
XX Sequence 414 AA;
SQ

Query Match 67.8%; Score 1425.5; DB 6; Length 414;
Best Local Similarity 68.2%; Pred. No. 2.2e-128;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKQCMKYMKNQKCV 60
Dy 1 MGGNHSKPPVFDENEENFDFHFIQLRAIGKSGFGEVCIVQKNDTKQCMKYMKNQKCI 60
Qy 61 ERNEVRNVFKEIQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNNVHFK 120
Dy 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNNVHFE 120
Qy 121 ETVKLFICELVMDLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Dy 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVVKGAERASM 180
Qy 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHIRSSTSSKEIVHTF 238
Dy 181 AGTKPYMAPEVFQVMDRGPYSYPVDWWSLGITAYELLRGRPPYHISVTPIDEILNMF 240
Qy 239 ETTVTYPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGF 298
Dy 241 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLDHISQVPLADNMWDVAFKKALMPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKMDKCDSSQTCLLQHLDSVQK 357
Dy 301 VPNGRLNCDPTFELEEMILESPLHKKKRLAKNRSRDTGKSCPLNGHLQHCLETRE 360
Qy 358 EPIIFNREKVRNDRFNKQPNLALQTKDPQG----EDGQNNNL 396
Dy 361 EPIIFNREKLRQGGQSGQLLDTDSRGGGQAQSKLQDGCNNNL 403

RESULT 15
ADE38375
ID ADE38375 standard; protein; 414 AA.
XX
AC ADE38375;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human protein 3703 amino acid sequence.
XX
KW tumorigenic disorder; angiogenic disorder; aberrant gene expression;
KW aberrant protein activity; cytostatic; antithyroid; antidiabetic;
KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW prostatic cancer; Grave's disease; diabetic retinopathy; protein 3703.
XX
OS Homo sapiens.
XX
PN WO2003065006-A2.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2003; 2003WO-US002588.
XX
PR 31-JAN-2002; 2002US-0353600P.
PR 15-MAR-2002; 2002US-0364517P.
PR 09-APR-2002; 2002US-0371075P.
PR 10-APR-2002; 2002US-0371507P.
PR 16-APR-2002; 2002US-0372984P.
PR 19-APR-2002; 2002US-0374194P.
PR 24-MAY-2002; 2002US-0382995P.
PR 31-MAY-2002; 2002US-0385023P.
PR 14-JUN-2002; 2002US-0388533P.
PR 17-JUN-2002; 2002US-0389395P.
PR 25-JUN-2002; 2002US-0391324P.
PR 15-JUL-2002; 2002US-0395944P.
PR 22-JUL-2002; 2002US-0397726P.

PR 13-AUG-2002; 2002US-0403046P.
PR 22-AUG-2002; 2002US-0405155P.
PR 27-AUG-2002; 2002US-0406361P.
PR 25-OCT-2002; 2002US-0421195P.
PR 12-NOV-2002; 2002US-0425456P.
PR 19-NOV-2002; 2002US-0427626P.
PR 10-DEC-2002; 2002US-0432122P.
XX (MILL-) MILLENNIUM PHARM INC.
PA Hunter JJ, Macbeth KJ, Taai F, Lesoon A, Lightcap ES;
PI Williamson MW, Rudolph-Owen LA;
XX WPI; 2003-646176/61.
DR N-PSDB; ADE38374.
XX
PT Treating subject having tumorigenic disorder or angiogenic disorder
PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
PT acid, by administering a modulator.
XX
PS Disclosure; SEQ ID NO 36; 454pp; English.
XX
CC This invention relates to a novel method of treating a human subject
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC gene expression or activity of an isolated protein, by administering a
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC or ophthalmological activity. The method is useful for treating a subject
CC having a tumorigenic or angiogenic disorder, in particular for treating
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC present sequence is the amino acid sequence of the novel isolated human
CC protein 3703 of the invention.
XX
SQ Sequence 414 AA;

Query Match 67.8%; Score 1425.5; DB 7; Length 414;
Best Local Similarity 68.2%; Pred. No. 2.2e-128;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKQCMKYMKNQKCV 60
Dy 1 MGGNHSKPPVFDENEENFDFHFIQLRAIGKSGFGEVCIVQKNDTKQCMKYMKNQKCI 60
Qy 61 ERNEVRNVFKEIQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNNVHFK 120
Dy 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNNVHFE 120
Qy 121 ETVKLFICELVMDLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Dy 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVVKGAERASM 180
Qy 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHIRSSTSSKEIVHTF 238
Dy 181 AGTKPYMAPEVFQVMDRGPYSYPVDWWSLGITAYELLRGRPPYHISVTPIDEILNMF 240
Qy 239 ETTVTYPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGF 298
Dy 241 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLDHISQVPLADNMWDVAFKKALMPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKMDKCDSSQTCLLQHLDSVQK 357
Dy 301 VPNGRLNCDPTFELEEMILESPLHKKKRLAKNRSRDTGKSCPLNGHLQHCLETRE 360
Qy 358 EPIIFNREKVRNDRFNKQPNLALQTKDPQG----EDGQNNNL 396
Dy 361 EPIIFNREKLRQGGQSGQLLDTDSRGGGQAQSKLQDGCNNNL 403

Search completed: June 25, 2004, 10:49:07
Job time : 62 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:55:12 ; Search time 2826 Seconds
(without alignments)
15691.910 Million cell updates/sec

Title: US-10-667-442-1
Perfect score: 1485
Sequence: 1 ccatgggagcgacacttca.....taaaaaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	968	65.2	1927	11 AK042599	AK042599 Mus muscu
2	968	65.2	2477	11 AK044474	AK044474 Mus muscu
3	968	65.2	3766	11 AK036266	AK036266 Mus muscu
4	710.6	47.9	893	10 BG036777	BG036777 602286992

5	555.2	37.4	3439	11 AK082468	AK082468 Mus muscu
6	553.6	37.3	1245	29 AY406286	AY406286 Mus muscu
7	540.8	36.4	1245	29 AY406284	AY406284 Homo sapi
8	533.8	35.9	1245	29 AY406285	AY406285 Pan trogl
9	494.4	33.3	2161	11 AK046439	AK046439 Mus muscu
10	466	31.4	829	13 BU156055	BU156055 AGENCOURT
11	455.2	30.7	836	13 BU412592	BU412592 603155332
12	426.8	28.7	869	10 BG033516	BG033516 602302120
13	421.6	28.4	1072	12 BM908009	BM908009 AGENCOURT
14	417.8	28.1	724	14 CB522564	CB522564 UI-M-GH0-
15	388.8	26.2	711	14 CA320851	CA320851 UI-M-FW0-
16	375.2	25.3	1003	13 BU146507	BU146507 AGENCOURT
17	372.8	25.1	995	13 BX401698	BX401698 BX401698
18	372.4	25.1	648	13 BY726568	BY726568 BY726568
19	365.6	24.6	664	10 BF472636	BF472636 UI-M-BH3-
20	364	24.5	1045	13 BX384945	BX384945 BX384945
21	361	24.3	1063	13 BQ925566	BQ925566 AGENCOURT
22	356.4	24.0	1201	13 BX416707	BX416707 BX416707
23	352.6	23.7	773	12 BI917132	BI917132 603181546
24	348.2	23.4	868	14 CF736437	CF736437 UI-M-HD0-
25	345.4	23.3	643	10 BB629092	BB629092 BB629092
26	341.2	23.0	667	10 BB642433	BB642433 BB642433
27	341	23.0	948	13 BX342288	BX342288 BX342288
28	340	22.9	862	10 BE567816	BE567816 601340485
29	333.2	22.4	1000	12 BG824303	BG824303 602727322
30	320.2	21.6	1055	13 BX384918	BX384918 BX384918
31	314.8	21.2	769	13 BQ571307	BQ571307 UI-M-FC0-
32	305.6	20.6	449	12 BQ044851	BQ044851 UI-M-EH0p
33	294.4	19.8	851	14 CA454976	CA454976 AGENCOURT
34	290.8	19.6	725	14 CD578874	CD578874 UI-M-GM0-
35	289.2	19.5	869	12 BG719068	BG719068 602699189
36	280.6	18.9	626	14 CA327599	CA327599 UI-M-FY0-
37	255.4	17.2	438	9 AI430616	AI430616 me09f10.y
38	254.2	17.1	451	14 W65887	W65887 me09f10.r1
39	253.6	17.1	441	13 BY289551	BY289551 BY289551
40	250	16.8	600	13 BX855511	BX855511 BX855511
41	247	16.6	578	12 BM934086	BM934086 UI-M-CG0p
42	245.2	16.5	1201	13 BX362859	BX362859 BX362859
43	238.8	16.1	778	14 CB520836	CB520836 UI-M-GH0-
44	233.8	15.7	639	13 BU320918	BU320918 603488113
45	233.4	15.7	365	10 BE947841	BE947841 UI-M-BH3-

ALIGNMENTS

RESULT 1
AK042599
LOCUS
DEFINITION
AK042599 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730009C22 product:SIMILAR TO SERINE
THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.
1927 bp mRNA linear HTC 19-SEP-2003
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
AK042599
AK042599.1 GI:26335202
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3766)
AUTHORS
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,P., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES
Location/Qualifiers
source
1. .3766
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evidence: PASTY, 95.5%ID, 94.5%length, match=471)
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ORIGIN
Query Match 65.2%; Score 968; DB 11; Length 3766;
Best Local Similarity 80.9%; Pred. No. 2.5e-172;
Matches 1218; Conservative 0; Mismatches 245; Indels 43; Gaps 6;
QY 1 CCATGGGAGCGAACACCTTCAAGAAACACCACAGTGTGTTGATGAAAAATGAAGATGTCAACT 60
Db 241 CCATGGGAGCGAACACCTTCAAGCAAAAGCCCCAGTGTGTTGATGAAAAATGAAGACGTCAACT 300
QY 61 TTGACCACCTTTGAAATTTTGGCAGCCATTGGGAAAGGCAGTTTGGGGAGGCTGTGCATTG 120
Db 301 TTGACCACCTTTGAAATTTTGGCAGCCATTGGGAAAGGCAGTTTGGGAAGGCTGTGCATTG 360
QY 121 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGC 180
Db 361 TGGCGAAGAATGACACCAAGAAGATGTACGCCATGAAGTACATGAACAACAAGAAGTGTG 420
QY 181 TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACCTCCAGATCATGCAGGGTCTGGAGC 240
Db 421 TGGAGCGGAATGAAGTGAGGAATGTCTTCAAGGAACCTCCAGATCATGCAGGGCCTGGAGC 480
QY 241 ACCCTTCTCTGGTAAATTTGTGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGGTGG 300
Db 481 ACCCTTCTCTGGTAAATCTGTGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGGTGG 540
QY 301 TGGACCTCTCTGGTGGGAGACCTGCGTTATCACCTGCAACAGAACGTCCTCAAGG 360
Db 541 TGGACCTCTCTGCTCGGTGGTGAATGAAACCTGCAATATTTTACTTGAATGAAATGTTCCAGG 600
QY 361 AAGAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAAC 420
Db 601 AGGACACAGTGAAGCTCTTTCATCTGTGAGCTGGCCATGGCCCTGGACTACCTACAGAGCC 660
QY 421 AGCGATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGAACAAATGTTGGCAGC 480
Db 661 AGCGATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGAATGAAATGTTGGCAGC 720
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Db 721 TGCATATCACAGACTTCAACATGTCTGCGATGTGCTGCCAGGAGACCCCGGATCACCACCG 780
QY 541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTTCAGTCCAGAAAGGAGCAGGCT 600
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QY 601 ATTCTTTTGTCTGTGACTGCTGCTCCCTGGGAGTGAACGATGATGAACTGCTGAGAGGCC 660
Db 841 ACTCTTTTGTCTGTGACTGCTGCTCCCTGGGAGTGAACGATGATGAACTGCTGAGAGGCC 900
QY 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 720
Db 901 GGAGACCATATCATATCCGCTCCAGTACTTCCAGCAAGGAATTTGTGAAACATGTTTGAGA 960
QY 721 CGACTGTTGTAACCTTACCCCTTCTGCTGGTTCACAGGAAATGGTGTCACTTCTTAAAAAGC 780
Db 961 CAGCAATTTGTAACCTTACCCCTTCTGCTGGTTCACAGGAGATGGTATCCCTTCTTAAAAAGC 1020
QY 781 TACTCGAACCTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGT 840
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QY	303	GACCTCCTGCTGGGTGGAGACCTGCGTTATCACTGCAACAGAACGTCCACTTCAAGGAA	362
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QY	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGC---	599
Db	909	GCTGGCACGAAGCCCTACATGGCCCTGAAAGTCTTCCAGGTGTATGTGGATGGAGGCCCT	968
QY	600	---TATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGA	656
Db	969	GGGTACTCATACCCCGTGGACTGGTGGTCACTGGGTGTACAGCCCTATGAGCTGCTCCGA	1028
QY	657	GGCCGGAGACCGTATCATATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTT	716
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QY	777	AAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC	836
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QY	897	ATTCTTAATAAAGGCAGGCTGAATTTGTATCCTACCTTTGAACCTTGAGGAAATGATTTTG	956
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QY	957	GAGTCCAAACCTCTACATAAGAAAAAAGCGTCTGGCAAAG---AAGGAGAAGGATATG	1013
Db	1329	GAATCCAAAGCCACTTTCACAAAAGAGAGAGGTTGGCCAAAGCATAGGTCCAGAGACAGC	1388
QY	1014	AGGAAATGCGATTTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAG	1073
Db	1389	ACAAAGGACAGCTGTCCCTGAAATGGACACCTGACAGAGTGTTTGGAGACAGTGGCGAAA	1448
QY	1074	GAGTTTCATAATTTTCAACAGAGAAAAAGTAAACAGGGA	1111
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RESULT 6	
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LOCUS	AY406286 1245 bp DNA linear GSS 12-DEC-2003
DEFINITION	Mus musculus HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY406286
VERSION	AY406286.1 GI:39762260
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1245)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Db 661 GGCTGGAGGCCATATGAGATCCACTCAGCCACACCCATTGATGAGATTCTCAACATGTTT 720
Qy 717 GAGACGACTGTTGTAACCTTACCCCTTCTGCTGTCAGAGAAATGGTGTCTACTTCTTAAA 776
Db 721 AAGGTGGAGCGTGTCCACTACTCTCCACGCTGGTGTGAGGGGATGGTGTCTCTGCTGAAG 780
Qy 777 AAGCTACTCGAACCTATATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC 836
Db 781 AAGCTGCTGACCAAGGACCTGAGAGCCGCTTGTCAAGTCTTCGTGACATCCAGAGCATG 840
Qy 837 CCGTATATGAATGATATAAAGTGGGATGCAGTTTTTTCAGAAAGGCTCATTCAGAGTTTC 896
Db 841 ACCTACCTGGCTGACATGAAGTGGGATGCAGTATTCGAGAAGGCCCTGATGCCTGGCTTT 900
Qy 897 ATTCTTAATAAAGCGAGCTGAATTTGTATCCTTACCTTTGAACCTTGAGGAATGATTTTG 956
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Qy 957 GAGTCCAAACCTCTACATAAGAAAAAAGCGTCTGSCAAAAG--AAGGAGAGGATATG 1013
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Qy 1014 ACGAATGCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAG 1073
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Db 1081 GAGTTCATCATATTCAACCGAGAGAAACTCAGGAGGCA 1118

RESULT 7
AY406284
LOCUS
DEFINITION Homo sapiens HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406284
VERSION AY406284.1 GI:39762258
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1245)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Best Local Similarity 69.1%; Pred. No. 7.9e-92;
Matches 772; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
Qy 3 ATGGGAGCGAACACATTCAAGAAAAACCCACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
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Db 1081 GAATTCATCATATTTCAACAGAGAGAAAGCTCAGGAGGCA 1118

RESULT 8

AY406285

LOCUS

DEFINITION Pan troglodytes HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406285

VERSION AY406285.1 GI:39762259

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 1245)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1245)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

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gene

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Best Local Similarity 68.2%; Pred. No. 1.6e-90;

Matches 762; Conservative 0; Mismatches 347; Indels 9; Gaps 2;

QY 3 ATGGGAGCGAACAACCTTCAAGAAACCAACACCACTGTTTGTATGAATAATGAAGATGTCAACTTT 62

Db 1 ATGGGCGGAACCACTCCACAAAGCCCCCGTGTGACGAGAAATGAGGAAGTCAACTTT 60

QY 63 GACCACCTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCATTGTA 122

Db 61 GACCATTTCAGATTCTGCGGGCCATTGGTAAGGGAGTTTGGAAAGGTATGCATCGTG 120

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Db 181 GAGAGGATGAGGTTTCGGAATGTCTTCGGGAGCTGCAGATCATGCAAGGGCTGGAGCAC 240

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Db 301 GACCTGCTCTCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCAATTTTCACAGAG 360

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QY 423 CGCATCATTCACAGGGATATGAAGCTGACAAATATTTTACCTTGACGAACATGGGCACGTG 482

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QY 483 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542

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QY 600 ---TATTCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGGATATGAATGCTGAGA 656

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QY 1074 GAGTTCATAATTTTCAACAGAGAAAAAGTAAACAGGGA 1111

Db 1081 GAATTCATCATATTTCAACAGAGAGAAAGCTCAGGAGGCA 1118

RESULT 9

AK046439

LOCUS

DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230385A21 product:hypothetical serine/threonine protein kinase, full insert sequence.

ACCESSION AK046439

VERSION AK046439.1 GI:26338088

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

AK046439

2161 bp

mrna

linear

HTC 20-SEP-2003

PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2161)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
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Best Local Similarity 67.2%; Pred. No. 3.5e-83;
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VERSION BU156055.1 GI:22669587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 829)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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551 TGGACCTCTCTGGTGGAGACCTGCGTTATTCACCTGCAACAGAACGTCACCTTCAAGG 610
QY 361 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGGCCCTGACTACCTGCAGAAC 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
611 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGGCCCTGACTACCTGCAGAAC 670
QY 421 AGCGCATCATTCACAGGGATATGAGCCTGACAAATATTTTACTTGACGAACATG 474
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
671 AGCGCATCATTCACAGGGATATGAGCCTGACAAATATTTTACTTGACGAACATG 724
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RESULT 11

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BU412592 836 bp mRNA linear EST 29-NOV-2002
LOCUS 603155332F1 CSEQRBL05 Gallus gallus cDNA clone ChEST168p8 5', mRNA
DEFINITION sequence.
ACCESSION BU412592
VERSION BU412592.1 GI:25905263
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 836)
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLES A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="ChEST168p8"
/sex="Female"
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FEATURES

source

Location/Qualifiers


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RESULT 13
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DEFINITION
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  5', mRNA sequence.
BM908009
BM908009.1 GI:19358388
EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1072)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
AUTHORS
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12767 row: c column: 18
High quality sequence stop: 692.
FEATURES
  Location/Qualifiers
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      /db_xref="taxon:9606"
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      /lab_host="DH10B"
      /clone_lib="NIH_MGC_119"
      /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
      Site_2: EcoRV (destroyed); RNA source normal medulla from
      anonymous male age 27. Library is oligo-dT primed and
      directionally cloned (EcoRV site is destroyed upon
      cloning). Average insert size 1.3 kb, insert size range
      0.9-3 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (Invitrogen). Research Genetics tracking code 013. Note:
      this is a NIH_MGC Library."
ORIGIN
  Query Match 28.4%; Score 421.6; DB 12; Length 1072;
  Best Local Similarity 69.4%; Pred. No. 2.2e-69;
  Matches 602; Conservative 0; Mismatches 257; Indels 8; Gaps 2;

  QY 3 ATGGGAGCGAACACTTCAAGAAAACCCACGAGTGTGTTGATGAAAATGAAGATGTCAACTTT 62
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  QY 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTTTGGGGAGGTCTGCATTGTA 122
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  Db 119 GACCACTTTTCAGATTTCTGCGGGCCATTGGTAAAGGGAGTTTTTGGAAAAGGTATGCATCGTG 178
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  QY 123 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCCTG 182
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  Db 179 CAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATC 238
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  QY 183 GAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATCGAGGCTCGGAGCAC 242
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  Db 239 GAGAGGATGAGGTTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGAGCAC 298
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  QY 243 CCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGGTG 302
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  Db 299 CCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGTGGTG 358
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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/clone="IMAGE:6842871"
/tissue_type="Whole brain"
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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ORIGIN

Query Match 28.1%; Score 417.8; DB 14; Length 724;
Best Local Similarity 78.4%; Pred. No. 1.3e-68;
Matches 561; Conservative 0; Mismatches 128; Indels 27; Gaps 4;

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QY 746 CTGCTCACAGGAAATGGTGTCACTTCTTAAAGAGCTACTCGAACCTTAATCCAGACCAACG 805
Db 129 CTGCTCACAGGAGATGGTATCCCTTCTTAAAGAGCTGCTGAACCTTAATCCAGACCAACG 188

QY 806 ATTTTCTCAGTTATCTGATGCTGCAGAACTTCCCGTATATGAATGATATAAACTGGGATGC 865
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QY 866 AGTTTTTCAGAAAGGCTCATTCAGGTTTCATTCCTTAATAAGGCGAGGCTGAATGTGA 925
Db 249 CGTCTGCAGAAAGGCTCATTCAGGCTTCATTCGACCAAGGCGAGGCTCAATGTGA 308

QY 926 TCCTACCTTTGAACCTTGAGGAATGATTTGGAGTCCCAACCTCTACATAAGAAAAAAA 985
Db 309 CCCCACTTTGAACCTTGGAAGAAATGATTTGGAGTCCCAACCTCTTCAAGAAAAAGAA 368

QY 986 GCGTCTGGCAAGAGGAGATATGAGGAAATGCGATTTCTTCTCAGACATGCTTCT 1045
Db 369 ACGACTGGCTAAAGGAGGAGAAATGAAGAAAGTGAAGTCTCTCTCAGACGCTGCTTCT 428

QY 1046 TCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCATAATTTTCAACAGAGAAAAAGTAAA 1105
Db 429 TCAAGAGCATCTTGATGCTGTTCAGAAAGAAATTTATATTTTCAACAGAGAAAAAGTAAA 488

QY 1106 CAGGAGCTTTAACAAGACAAACCAATCTAGCCTTGGAAACCAACCAAGAC-----CC 1159
Db 489 AAGTGACTTTAATCAGAGACAAAGCAAAATCTAGCCTTGGAAACCAACCAACCAAGAC 548

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Db 549 AGAGGAGGAGGAGCGGCCAGATAAACAACCTATAAAGTGTCTCCGAGTCTTCGGGGGACAG 608

QY 1206 TTTCTTCTGGGACAAT-----CTCATGCCAGAACTTCTTAATTACATATGTCAAGAAAA 1259
Db 609 TGCTTCGGGGACAGTTCTTGGCACTTGGCGGGAAGTCTCTGATTTATCACACACAGAGA 668

QY 1260 GCTGACAGTAGCTCTGCCACT-CCACACACCATGACTTAGAAAAATGTGAATGAAT 1314
Db 669 GCTGACAGGAGTCTGCTGCCACTGCCACACCTCATGACTTAGAGAAATATGAATGAGT 724
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RESULT 15
CA320851
LOCUS

DEFINITION UI-M-FW0-ccb-b-18-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6817171 5', mRNA sequence.

ACCESSION CA320851
VERSION CA320851.1 GI:24538949
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 711)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers
1. 711
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

FEATURES
source

Location/Qualifiers

1. 711

/organism="Mus musculus"

/mol_type="mRNA"

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/clone="IMAGE:6817171"

/tissue_type="whole brain"

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/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 26.2%; Score 388.8; DB 14; Length 711;
Best Local Similarity 72.8%; Pred. No. 3.7e-63;
Matches 517; Conservative 0; Mismatches 187; Indels 6; Gaps 1;

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Db 1 GAGATCCTCGCGGCCATTGGGAAGGGAAGTTTGGAAAGGTATGTCATCGTCGAGAGCGA 60

QY 132 GATACCAAGAGATGTCGCAATGAAGTACATGAATAAACAAAGTCCGTGGAGCGCAAT 191
Db 61 GACACAAAGAGATGTCGCAATGAAGTACATGAATGAAGTGTGTGAGAGGGAT 120

QY 192 GAAGTGAGAAATGCTTCAAGGAACCTCCAGATCATGAGGGTCTGGAGCACCTTCTCTG 251
Db 121 GAGGTGCGGAACGTTTCGGGAGCTGCAGATCATGAGGGATTAGAGCACCTTCTCTG 180
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 22:20:22 ; Search time 500 Seconds
(without alignments)
13605.835 Million cell updates/sec

Title: US-10-667-442-1
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Scoring table: IDENTITY NUC
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Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1485	100.0	1485	13	US-10-667-442-1
3	1485	100.0	1485	15	US-10-254-869-1
4	1228.6	82.7	1281	16	US-10-410-764-100
5	1188.2	80.0	1594	13	US-10-362-892-44
6	1188.2	80.0	1594	13	US-10-182-243-1
7	1188.2	80.0	1594	16	US-10-288-798-44
8	1186.2	79.9	1191	9	US-09-841-683-10
9	1184.6	79.8	1191	16	US-10-410-764-102
10	1162.6	78.3	1675	9	US-09-841-683-12
11	1160.6	78.2	1224	9	US-09-841-683-8
12	1029.4	69.3	2063	16	US-10-108-260A-231
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14	656.2	44.2	711	9	US-09-841-683-6

15	655.2	44.1	678	9	US-09-841-683-4	Sequence 4, Appli
16	540.8	36.4	3224	13	US-10-342-887-1782	Sequence 1782, Ap
17	540.8	36.4	3224	13	US-10-172-118-1782	Sequence 1782, Ap
18	540.8	36.4	3224	15	US-10-161-803-40	Sequence 40, Appl
19	540.8	36.4	3224	15	US-10-354-358-35	Sequence 35, Appl
20	516.4	34.8	3244	13	US-10-206-915-571	Sequence 571, App
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ALIGNMENTS

RESULT 1

US-09-801-876B-1
; Sequence 1, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-09-801-876B-1

Query Match	100.0%;	Score 1485;	DB 9;	Length 1485;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1485;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCACTTTGGGAGGTCTGCATTG	120	
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Db	121	TACAGAAGATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAACAAAGTGC	180	
Qy	181	TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCGGTCTGGAGC	240	

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Db 707 GGAGACGGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 766
QY 721 CGACTGTTGTAACTTACCCTTCTGCTGGTCCAGGAAATGGTGTCACTTCTTAAAGAAGC 780
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QY 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
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QY 841 ATATGAATGATATAAACTGGGATGCAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTC 900
Db 887 ATATGAATGATATAAACTGGGATGCAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTC 946
QY 901 CTAATAAAGGCGAGCTGAATTTGTGATCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGT 960
Db 947 CTAATAAAGGCGAGCTGAATTTGTGATCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGT 1006
QY 961 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1020
Db 1007 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1066
QY 1021 GCGATTCTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTCA 1080
Db 1067 GCGATTCTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTCA 1126
QY 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGGAGCTTTTAAACAAAAGACAACTTCTAGCCT 1140
Db 1127 TAATTTTCAACAGAGAAAAAGTAAACAGGGAGCTTTTAAACAAAAGACAACTTCTAGCCT 1186
QY 1141 TGGAAACAAACCAAGACCCACAAAGGTGAGGATGGTCAAGATTAACAACTTGTAAAGGCCTC 1200
Db 1187 TGGAAACAAACCAAGACCCACAAAGGTGAGGATGGTCAAGATTAACAACTTGTAAAGGCCTC 1246
QY 1201 ATGTCTTCTTCTTGGGACAAATCTCATGCGCAGAAAC 1235
Db 1247 ATGTCTTCTTCTTGGGACAAATCTCATGCGCAGAAAC 1281

RESULT 5

US-10-362-892-44
; Sequence 44, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Dannel B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CB1
US-10-362-892-44

Query Match 80.0%; Score 1188.2; DB 13; Length 1594;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGGGAGCGAACACTTCAAGAAAAACCACCACTGTTGATGAAAAATGAAGATGTCAACT 60
Db 402 CCATGGGAGCGAACACTTCAAGAAAAACCACCACTGTTGATGAAAAATGAAGATGTCAACT 461
QY 61 TTGACCACCTTTGAAATTTTGGAGGCCATTGGGAAAGGCAGTTTGGGGAGGCTCTGCATTG 120
Db 462 TTGACCACCTTTGAAATTTTGGAGGCCATTGGGAAAGGCAGTTTGGGGAGGCTCTGCATTG 521
QY 121 TACAGAAAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
Db 522 TACAGAAAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 581
QY 181 TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACCTCAGATCATGCAGGGTCTGGAGC 240
Db 582 TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACCTCAGATCATGCAGGGTCTGGAGC 641
QY 241 ACCCTTTCTGTTAATTTGTGGTATTCTTCCAAGATGAGGAAGACATGTTTCATGTTGG 300
Db 642 ACCCTTTCTGTTAATTTGTGGTATTCTTCCAAGATGAGGAAGACATGTTTCATGTTGG 701
QY 301 TGGACCTCTGCTGGGTGAGACCTGCGTTATCACCTGCAACAGAACCTCCACTTCAAGG 360
Db 702 TGGACCTCTGCTGGGTGAGACCTGCGTTATCACCTGCAACAGAACCTCCACTTCAAGG 761
QY 361 AAGAAACAGTGAAGCTTTCATCTGTGAGCTGGTCAATGCGCCCTGGACTACCTGCAGAAC 420
Db 762 AAGAAACAGTGAAGCTTTCATCTGTGAGCTGGTCAATGCGCCCTGGACTACCTGCAGAAC 821
QY 421 AGCGCATCATTCACAGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACG 480
Db 822 AGCGCATCATTCACAGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACG 881
QY 481 TGCACATCACAGATTTCAACATTTGCGATGCTGCCAGGAGACACAGATTACCA 540
Db 882 TGCACATCACAGATTTCAACATTTGCGATGCTGCCAGGAGACACAGATTACCA 941
QY 541 TGGCTGGCACCACCAAGCCTTACATGGCACCTGAGATGTTTCCAGAAAAGGAGCAGGCT 600
Db 942 TGGCTGGCACCACCAAGCCTTACATGGCACCTGAGATGTTTCCAGAAAAGGAGCAGGCT 1001
QY 601 ATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGSCATATGAACTGCTGAGAGGCC 660
Db 1002 ATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGSCATATGAACTGCTGAGAGGCC 1061
QY 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 720
Db 1062 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 1121

QY 721 CGACTGTTGTAACTTACCTTCTGCCTGGTCAAGGAAATGGTGTCACTTCTTAAAGC 780
DB 1122 CGACTGTTGTAACTTACCTTCTGCCTGGTCAAGGAAATGGTGTCACTTCTTAAAGC 1181
QY 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 840
DB 1182 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 1241
QY 841 ATATGAATGATATAAATCGGATGCGATTTTTCAGAAAGGCTCATTCAGGTTTCATTC 900
DB 1242 ATATGAATGATATAAATCGGATGCGATTTTTCAGAAAGGCTCATTCAGGTTTCATTC 1301
QY 901 CTAATAAAGGCGAGGCTGAATTTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGT 960
DB 1302 CTAATAAAGGCGAGGCTGAATTTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGT 1361
QY 961 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAAT 1020
DB 1362 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAAT 1421
QY 1021 GCGATTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAAAGGATTC 1080
DB 1422 GCGATTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAAAGGATTC 1481
QY 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCT 1140
DB 1482 TAATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCT 1541
QY 1141 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1193
DB 1542 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1594

RESULT 6

US-10-182-243-1
; Sequence 1, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-243-1

Query Match 80.0%; Score 1188.2; DB 13; Length 1594;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCATGGGAGCGAACACTTCAAGAAAAACCAAGTGTGATGAAATGAAGATGTCAACT 60
DB 402 CCATGGGAGCGAACACTTCAAGAAAAACCAAGTGTGATGAAATGAAGATGTCAACT 461
QY 61 TTGACCACCTTGAATTTTGGAGGCCATTTGGAAAGGCGATTTTGGGGAGGCTCTGCATTG 120
DB 462 TTGACCACCTTGAATTTTGGAGGCCATTTGGAAAGGCGATTTTGGGGAGGCTCTGCATTG 521
QY 121 TACAGAAAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATATAACAAAGTGG 180
DB 522 TACAGAAAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATATAACAAAGTGG 581

QY 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGAGGGTCTGGAGC 240
DB 582 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGAGGGTCTGGAGC 641
QY 241 ACCCTTCTCTGGTTAATTTGTGGTATCTCTTCAAGATGAGGAAAGACATGTTTCAAGG 300
DB 642 ACCCTTCTCTGGTTAATTTGTGGTATCTCTTCAAGATGAGGAAAGACATGTTTCAAGG 701
QY 301 TGGACCTCTCTGGTTGAGGACCTGCGTATCACCTGCAACAGAACCTCCACTTCAAGG 360
DB 702 TGGACCTCTCTGGTTGAGGACCTGCGTATCACCTGCAACAGAACCTCCACTTCAAGG 761
QY 361 AAGAAACAGTGAAGCTCTTCTCATCTGTGAGTGGTCAATGAGGCTGAGGAGGAGGAGG 420
DB 762 AAGAAACAGTGAAGCTCTTCTCATCTGTGAGTGGTCAATGAGGCTGAGGAGGAGGAGG 821
QY 421 AGCGCATCATTCACAGGATATGAAGCTTGACCAATATTTTACTTTCGCAACATGGGCACG 480
DB 822 AGCGCATCATTCACAGGATATGAAGCTTGACCAATATTTTACTTTCGCAACATGGGCACG 881
QY 481 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCGGAGGAGACACAGATTACCACCA 540
DB 882 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCGGAGGAGACACAGATTACCACCA 941
QY 541 TGGCTGGCACCAAGCTTACATGATGGACCTGAGATGTTTCAAGTCCAGAAAGGAGGAGG 600
DB 942 TGGCTGGCACCAAGCTTACATGATGGACCTGAGATGTTTCAAGTCCAGAAAGGAGGAGG 1001
QY 601 ATTCTTTGCTGTGAGTGGTGGTCTGCGGAGTGGAGGATATGAACTGCTGAGAGGCGC 660
DB 1002 ATTCTTTGCTGTGAGTGGTGGTCTGCGGAGTGGAGGATATGAACTGCTGAGAGGCGC 1061
QY 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGCTTTGAGA 720
DB 1062 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGCTTTGAGA 1121
QY 721 CGACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 1122 CGACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
QY 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 840
DB 1182 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 1241
QY 841 ATATGAATGATATAAATCGGATGCGATTTTTCAGAAAGGAGGCTCATTCAGGTTTCATTC 900
DB 1242 ATATGAATGATATAAATCGGATGCGATTTTTCAGAAAGGAGGCTCATTCAGGTTTCATTC 1301
QY 901 CTAATAAAGGCGAGGCTGAATTTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGT 960
DB 1302 CTAATAAAGGCGAGGCTGAATTTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGT 1361
QY 961 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAAT 1020
DB 1362 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAAT 1421
QY 1021 GCGATTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTC 1080
DB 1422 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTC 1481
QY 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCT 1140
DB 1482 TAATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCT 1541
QY 1141 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1193
DB 1542 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1594

RESULT 7
US-10-288-798-44
; Sequence 44, Application US/10288798

; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-10

Query Match 79.9%; Score 1186.2; DB 9; Length 1191;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGAGCGAACAATTCAAGAAACACCAAGTGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 182
Db 1 ATGGAGCGAACAATTCAAGAAACACCAAGTGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 180

Qy 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTGCGATTGTA 122
Db 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTGCGATTGTA 120

Qy 123 CAGAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 182
Db 121 CAGAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 180

Qy 183 GAGCGCAATGAAGTGAAGTGTCTTCAAGGAACCTCCAGATCATGCAGGCTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAAGTGTCTTCAAGGAACCTCCAGATCATGCAGGCTCTGGAGCAC 240

Qy 243 CCTTCTCTGGTTAATTTGTGGTATCTTCCAGATGAGGAAGACATGTTTCATGGTGGTG 302
Db 241 CCTTCTCTGGTTAATTTGTGGTATCTTCCAGATGAGGAAGACATGTTTCATGGTGGTG 300

Qy 303 GACCTCTCTGGTGGTGAGACCTGGCTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 362
Db 301 GACCTCTCTGGTGGTGAGACCTGGCTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360

Qy 363 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGAGGCTGAGTACCTGCAAGAACAG 422
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGAGGCTGAGTACCTGCAAGAACAG 420

Qy 423 CGATCATTCACAGGATATGAAGCTGACAAATATTTTACTTACGAAACATGGGCACTG 482
Db 421 CGATCATTCACAGGATATGAAGCTGACAAATATTTTACTTACGAAACATGGGCACTG 480

Qy 483 CACATCACAGATTTCAACATTGTGCGATGCTGCCAGGAGACACAGATTACCAACATG 542
Db 481 CACATCACAGATTTCAACATTGTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540

Qy 543 GCTGGCAACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGCTAT 602
Db 541 GCTGGCAACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGCTAT 600

Qy 603 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGGATATGAATGCTGAGAGGCGG 662
Db 601 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGGATATGAATGCTGAGAGGCGG 660

Qy 663 AGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGCTTTGAGAGG 722
Db 661 AGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGCTTTGAGAGG 720

Qy 723 ACTGTTGTAACCTTACCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGCTA 782
Db 721 ACTGTTGTAACCTTACCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGCTA 780

Qy 783 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACCTCCCGTAT 842
Db 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACCTCCCGTAT 840

RESULT 9

US-10-410-764-102
; Sequence 102, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520NMIM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 1191
; TYPE: DNA

Qy 843 ATGAATGATATAAACTGGGATGCAGTTTTTTCAGAAAGGGCTCATTCAGGTTTCATTCCT 902
Db 841 ATGAATGATATAAACTGGGATGCAGTTTTTTCAGAAAGGGCTCATTCAGGTTTCATTCCT 900

Qy 903 AATAAAGGCGAGCTGAATTGTGATCCTACCTTTGAACTTGGAGAAATGATTTGGAGTCC 962
Db 901 AATAAAGGCGAGCTGAATTGTGATCCTACCTTTGAACTTGGAGAAATGATTTGGAGTCC 960

Qy 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAATGC 1022
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAAAGGAGGATATGAGGAAATGC 1020

Qy 1023 GATTCTTCTCAGACATGTCTTCTTCAAGAGGACCTTGACTCTGTCCAGAGGAGTTTCATA 1082
Db 1021 GATTCTTCTCAGACATGTCTTCTTCAAGAGGACCTTGACTCTGTCCAGAGGAGTTTCATA 1080

Qy 1083 ATTTTCAACAGAAAAAGTAAACAGGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1142
Db 1081 ATTTTCAACAGAAAAAGTAAACAGGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140

Qy 1143 GAACAAACCAAGACCCCAAGGTGAGGATGGTTCAGATAACAACTTGTAA 1193
Db 1141 GAACAAACCAAGACCCCAAGGTGAGGATGGTTCAGATAACAACTTGTAA 1191

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1191)
US-10-410-764-102

Query Match 79.8%; Score 1184.6; DB 16; Length 1191;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1187; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ATGGGAGCGAACACATTCAAGAAACCACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAACACATTCAAGAAACCACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60

Qy 63 GACCACATTGAAATTTTGGAGCCATTGGGAAAGGCAGTTTGGGAGGTTCTGCATTGTA 122
Db 61 GACCACATTGAAATTTTGGAGCCATTGGGAAAGGCAGTTTGGGAGGTTCTGCATTGTA 120

Qy 123 CAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGATGAATAAACAAGTCGGTG 182
Db 121 CAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGATGAATAAACAAGTCGGTG 180

Qy 183 GAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATGAGGGTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATGAGGGTCTGGAGCAC 240

Qy 243 CCTTCTCTGTTAATTGTGTTATTCCTTCCAAAGATGAGGAAGACATGTTTCATGGTGGTG 302
Db 241 CCTTCTCTGTTAATTGTGTTATTCCTTCCAAAGATGAGGAAGACATGTTTCATGGTGGTG 300

Qy 303 GACCTCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 362
Db 301 GACCTCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360

Qy 363 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGCGCCCTGGACTACCTGCAGAACCCAG 422
Db 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGCGCCCTGGACTACCTGCAGAACCCAG 420

Qy 423 CGCATCATTCACAGGGATATGAAGCCCTGACAATATTTTACTTGACGAACATGGGCACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCCCTGACAATATTTTACTTGACGAACATGGGCACGTG 480

Qy 483 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 542
Db 481 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGAGATACAGATTACCACCATG 540

Qy 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCCAGTCCAGAAAGGAGCAGGCTAT 602
Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCCAGTCCAGAAAGGAGCAGGCTAT 600

Qy 603 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 662
Db 601 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 660

Qy 663 AGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 722
Db 661 AGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 720

Qy 723 ACTGTTGTAACTTACCCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGGCTA 782
Db 721 ACTGTTGTAACTTACCCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGGCTA 780

Qy 783 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCCTAT 842
Db 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCCTAT 840

Qy 843 ATGAATGATATAAATCTGGGATGAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 902
Db 841 ATGAATGATATAAATCTGGGATGAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 900

Qy 903 AATAAGGCAGGCTGAATTTGTATCCTACCTTTGAACCTTGAGGAATGATTTTGGAGTCC 962
Db 901 AATAAGGCAGGCTGAATTTGTATCCTACCTTTGAACCTTGAGGAATGATTTTGGAGTCC 960

RESULT 10

US-09-841-683-12

; Sequence 12, Application US/09841683

; Patent No. US20020081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. US20020081600A1e1 Human Kinase Proteins and Polynucleotides

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 1675

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 9; Length 1675;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACACACTTCAAGAAACCACCAAGTGTGTTGATGAAATGAAGATGTCAACT 60
Db 411 CCATGGGAGCGAACACACTTCAAGAAACCACCAAGTGTGTTGATGAAATGAAGATGTCAACT 470

Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCAGTTTGGGGAGGTCTGCATTG 120
Db 471 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCAGTTTGGGGAGGTCTGCATTG 530

Qy 121 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
Db 531 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 590

Qy 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCAGGTCTGGAGC 240
Db 591 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCAGGTCTGGAGC 650

Qy 241 ACCCTTCTCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGG 300
Db 651 ACCCTTCTCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGG 710

Qy 301 TGGACCTCTCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG 360
Db 711 TGGACCTCTCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG 770

; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4

Query Match		44.1%	Score 655.2;	DB 9;	Length 678;
Best Local Similarity		99.5%;	Pred. No. 2.6e-187;		
Matches 657;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	3	ATGGGAGCGAACACCTTCAAGAAACACACCAGTGTGTTGATGAAATGAAGATGTCAACTTT	62		
Db	1	ATGGGAGCGAACACCTTCAAGAAACACACCAGTGTGTTGATGAAATGAAGATGTCAACTTT	60		
Qy	63	GACCACTTTGAAATTTTTCGAGCCATTGGGAAAGGCAGTTTGGGAGGCTCTGCATTGTA	122		
Db	61	GACCACTTTGAAATTTTTCGAGCCATTGGGAAAGGCAGTTTGGGAGGCTCTGCATTGTA	120		
Qy	123	CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG	182		
Db	121	CAGAAGAATGATACCAAGAAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG	180		
Qy	183	GAGCGCAATGAAGTGAGAAATGCTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGCAC	242		
Db	181	GAGCGCAATGAAGTGAGAAATGCTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGCAC	240		
Qy	243	CCTTCTCTGGTTAATTTGTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGGTG	302		
Db	241	CCTTCTCTGGTTAATTTGTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGGTG	300		
Qy	303	GACCTCTCTGGTGGAGACCTGGGTTATCACCTGCAACAGAACGTCCACITTCAGAGAA	362		
Db	301	GACCTCTCTGGTGGAGACCTGGGTTATCACCTGCAACAGAACGTCCACITTCAGAGAA	360		
Qy	363	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAACCCAG	422		
Db	361	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAACCCAG	420		
Qy	423	CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACTG	482		
Db	421	CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACTG	480		
Qy	483	CACATCACAGATTTCAACATTGTGCGGATGCTGCCAGGAGACACAGATTACCCATG	542		
Db	481	CACATCACAGATTTCAACATTGTGCGGATGCTGCCAGGAGACACAGATTACCCATG	540		
Qy	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGTCCAGAAAGGAGCAGGCTAT	602		
Db	541	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGTCCAGAAAGGAGCAGGCTAT	600		
Qy	603	TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATGCTGAGAGGCCGG	662		
Db	601	TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATGCTGAGAGGCCGG	660		

Search completed: June 27, 2004, 00:23:55
Job time : 504 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:58:26 ; Search time 95 Seconds
(without alignments) 8674.759 Million cell updates/sec

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Title:      US-10-667-442-1
Perfect score: 1485
Sequence: 1 ccattggagcggaacacttca.....taaaaaaaaaaaaaaaaa 1485

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1485	100.0	1485	4	US-09-801-876B-1		Sequence 1, Appli
2	1485	100.0	1485	4	US-10-254-869-1		Sequence 1, Appli
3	1186.2	79.9	1191	4	US-09-841-683-10		Sequence 10, Appl
4	1162.6	78.3	1675	4	US-09-841-683-12		Sequence 12, Appl
5	1160.6	78.2	1224	4	US-09-841-683-8		Sequence 8, Appli
6	656.2	44.2	711	4	US-09-841-683-6		Sequence 6, Appli
7	655.2	44.1	678	4	US-09-841-683-4		Sequence 4, Appli
8	481.6	32.4	1257	4	US-09-799-875-15		Sequence 15, Appl
9	481.6	32.4	1826	4	US-09-799-875-13		Sequence 13, Appl
10	466.8	31.4	1864	4	US-09-819-607-1		Sequence 1, Appli
11	363.4	24.5	148567	4	US-09-801-876B-3		Sequence 3, Appli
12	363.4	24.5	148567	4	US-10-254-869-3		Sequence 3, Appli
13	132.6	8.9	1008	4	US-09-394-455-3		Sequence 3, Appli
14	132.6	8.9	2549	3	US-09-467-082-3		Sequence 3, Appli
15	132.6	8.9	2549	4	US-09-394-455-5		Sequence 5, Appli
16	132.6	8.9	2608	4	US-09-394-455-35		Sequence 35, Appl
17	132	8.9	1619	4	US-09-394-455-14		Sequence 14, Appl
18	122.6	8.3	25603	4	US-09-819-607-3		Sequence 3, Appli
19	120.4	8.1	1498	4	US-09-509-902A-6		Sequence 6, Appli
20	120.4	8.1	1961	4	US-09-509-902A-15		Sequence 15, Appl
21	120.4	8.1	2204	1	US-08-221-817-12		Sequence 12, Appl
22	120.4	8.1	2204	1	US-08-454-439-12		Sequence 12, Appl
23	120.4	8.1	2204	5	PCT-US94-10487-12		Sequence 12, Appl
24	120.4	8.1	2206	1	US-08-221-817-10		Sequence 10, Appl
25	120.4	8.1	2206	1	US-08-454-439-10		Sequence 10, Appl
26	120.4	8.1	2206	5	PCT-US94-10487-10		Sequence 10, Appl
27	120.4	8.1	2848	3	US-08-464-954A-2		Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-801-876B-1

; Sequence 1, Application US/09801876B

; Patent No. 6492155

: GENERAL INFORMATION:

APPLICANT: YE, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MAPPING

FILE REFERENCE: CL001160

FILE REFERENCE: CEC001100
: CURRENT APPLICATION NUMBER: IIS/09/801 - 8768

; CURRENT AFFILIATION NUMBER: US/0
 : CURRENT FILING DATE: 2001-03-09

; CURRENT FILING DATE: 2
 : NUMBER OF SEC TO NOS: 8

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0

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SOFTWARE: . SEQ ID NO 1

: SEQ ID NO 1
: LENGTH: 1485

LENGTH: 1
TYPE: DNA

TYPE: DNA
ORGANISM: Human

;
ORGANISM: HU
IIC-09-801-9768-1

Query Match 100.0%; Score 1485; DB 4; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCATGGGAGCGGAACA	CTTCAAGAAAACCA	CCAGTGT	TTGATG	AAAAATGA	AGATGT	CAACT	60
Db	1	CCATGGGAGCGGAACA	CTTCAAGAAAACCA	CCAGTGT	TTGATG	AAAAATGA	AGATGT	CAACT	60
QY	61	TTGACCACTTTGAAAT	TTTTCGAGCCATT	GGGAAAGCGCAGT	TTTGGG	GAGGCTTG	CATTG	120	
Db	61	TTGACCACTTTGAAAT	TTTTCGAGCCATT	GGGAAAGCGCAGT	TTTGGG	GAGGCTTG	CATTG	120	
QY	121	TACAGAAAGAAATGAT	ATCAAGAAGATGT	GCGCAATGA	AGTACATGA	ATATAACA	AAAGTGCG	180	
Db	121	TACAGAAAGAAATGAT	ATCAAGAAGATGT	GCGCAATGA	AGTACATGA	ATATAACA	AAAGTGCG	180	
QY	181	TGGAGCGCAATGAAGT	GAGAAATGTCTT	CAAGAACTCC	CAGATCAT	GCAGGCTTG	GAGC	240	
Db	181	TGGAGCGCAATGAAGT	GAGAAATGTCTT	CAAGAACTCC	CAGATCAT	GCAGGCTTG	GAGC	240	
QY	241	ACCCTTTCCTGGTTAA	TTGTGGTATTCCTT	CAAGATGAG	GAAGACAT	GTTCAT	GGTGG	300	
Db	241	ACCCTTTCCTGGTTAA	TTGTGGTATTCCTT	CAAGATGAG	GAAGACAT	GTTCAT	GGTGG	300	
QY	301	TGGACCTCCTGCTGGG	TGGAGACCTGCGTT	ATCACTGCA	ACAGAACG	TCCACTT	CAAGG	360	
Db	301	TGGACCTCCTGCTGGG	TGGAGACCTGCGTT	ATCACTGCA	ACAGAACG	TCCACTT	CAAGG	360	
QY	361	AAGAAACAGTGAAGCT	CTTCATCTGT	GAGCTGGT	CATGGCCCT	TGAC	TACCTGC	420	

Db 901 AATAAGGCGAGGCTGAATGTGATCCTACCTTTGAACCTTGAGGAAATGATTTGGAGTCC 960
Qy 963 AAACCTCTACATAAGAAAAAAGCGCTGCGCAAGAGGAGGATATGAGGAAATGC 1022
Db 961 AAACCTCTACATAAGAAAAAAGCGCTGCGCAAGAGGAGGATATGAGGAAATGC 1020
Qy 1023 GATTCTTCTCAGACATGCTTCTTCAAGAGACCTTGACTCTGTCCAGAGGAGTTTATA 1082
Db 1021 GATTCTTCTCAGACATGCTTCTTCAAGAGACCTTGACTCTGTCCAGAGGAGTTTATA 1080
Qy 1083 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1142
Db 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
Qy 1143 GAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1193
Db 1141 GAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACAACTTGTAA 1191

RESULT 4

US-09-841-683-12

; Sequence 12, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 1675

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 4; Length 1675;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGATGAAATGAAGATGTCAACT 60
Db 411 CCATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGATGAAATGAAGATGTCAACT 470
Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAGGTCTGCATTG 120
Db 471 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAGGTCTGCATTG 530
Qy 121 TACAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGAGTGG 180
Db 531 TACAGAAGATGATACCAAGAGATGTGACGAATGAAGTACATGAATAAACAAGAGTGG 590
Qy 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCAGATCATGCAGGTCTGGAGC 240
Db 591 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCAGATCATGCAGGTCTGGAGC 650
Qy 241 ACCCTTCTCGTTAATTTGTGGTATTCCTTCAAGATGAGGAGACATGTTTCATGGTGG 300
Db 651 ACCCTTCTCGTTAATTTGTGGTATTCCTTCAAGATGAGGAGACATGTTTCATGGTGG 710
Qy 301 TGGACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCACCTTCAAGG 360

Db 711 TGGACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG 770
Qy 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 420
Db 771 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 830
Qy 421 AGCGCATATTCAAGGGATATGAAGCCTGACAATATTTTACTTACGAAACATGGGCACG 480
Db 831 AGCGCATATTCAAGGGATATGAAGCCTGACAATATTTTACTTACGAAACATGGGCACG 890
Qy 481 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACA 540
Db 891 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACA 950
Qy 541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGCT 600
Db 951 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGCT 1010
Qy 601 ATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC 660
Db 1011 ATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC 1070
Qy 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGA 720
Db 1071 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGA 1130
Qy 721 CGACTGTTGTAACCTTACCCCTTCTGCTGGTTCACAGGAAATGGTGTCTACTTCTTAAAAAGC 780
Db 1131 CGACTGTTGTAACCTTACCCCTTCTGCTGGTTCACAGGAAATGGTGTCTACTTCTTAAAAAGC 1190
Qy 781 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Db 1191 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 1250
Qy 841 ATATGAATGATATAAACTGGGATGAGTGTTCAGAAAGGCTCATTCAGAGTTTCAATTC 900
Db 1251 ATATGAATGATATAAACTGGGATGAGTGTTCAGAAAGGCTCATTCAGAGTTTCAATTC 1310
Qy 901 CTAATAAGGCGAGGCTGAATTTGTGATCTCTACCTTTGAACCTTGAAGAAATGATTTGGAGT 960
Db 1311 CTAATAAGGCGAGGCTGAATTTGTGATCTCTACCTTTGAACCTTGAAGAAATGATTTGGAGT 1370
Qy 961 CCAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGAGGATATGAGGAAAT 1020
Db 1371 CCAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGAGGATATGAGGAAAT 1430
Qy 1021 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTCA 1080
Db 1431 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTCA 1490
Qy 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAAATCTAGCCT 1140
Db 1491 TAATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAAATCTAGCCT 1550
Qy 1141 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACA 1185
Db 1551 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAAGATAACA 1595

RESULT 5

US-09-841-683-8

; Sequence 8, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-8

Query Match 78.2%; Score 1160.6; DB 4; Length 1224;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 3 ATGGAGCGAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGAGCGAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60

QY 63 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTGTGTTGGGAGGTCTGCAATTGA 122
Db 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTGTGTTGGGAGGTCTGCAATTGA 120

QY 123 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 182
Db 121 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 180

QY 183 GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATGCAGGTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATGCAGGTCTGGAGCAC 240

QY 243 CCTTCTCTGTTAAATTTGTGTTATCTTCAAGATGAGGAAGACATGTTTATGTTGGTG 302
Db 241 CCTTCTCTGTTAAATTTGTGTTATCTTCAAGATGAGGAAGACATGTTTATGTTGGTG 300

QY 303 GACCTCTGCTGGTGGAGACCTGCTTATCACCCTGCAACAGAACTCCACITCAAGGAA 362
Db 301 GACCTCTGCTGGTGGAGACCTGCTTATCACCCTGCAACAGAACTCCACITCAAGGAA 360

QY 363 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTTGCTGCTGCAAGTACCTGCAGAACAG 422
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTTGCTGCTGCAAGTACCTGCAGAACAG 420

QY 423 CGCATCATTCACAGGGATATGAAGCTGACAATATTTTACTTGACGAACATGGGACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCTGACAATATTTTACTTGACGAACATGGGACGTG 480

QY 483 CACATCACAGATTTCAACATTGCTGCGATGTGCTGCCAGGAGACACAGATTACCAATG 542
Db 481 CACATCACAGATTTCAACATTGCTGCGATGTGCTGCCAGGAGACACAGATTACCAATG 540

QY 543 GCTGGCACCAAGCCTTACATGGCACCCTGAGATGTTTCACTCCAGAAAGGAGCAGGTAT 602
Db 541 GCTGGCACCAAGCCTTACATGGCACCCTGAGATGTTTCACTCCAGAAAGGAGCAGGTAT 600

QY 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGAGTGACGGCATATGAATGAACTGCTGAGAGCGG 662
Db 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGAGTGACGGCATATGAATGAACTGCTGAGAGCGG 660

QY 663 AGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAATGTACACACGTTTGACAG 722
Db 661 AGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAATGTACACACGTTTGACAG 720

QY 723 ACTGTGTAACTTACCTTCTGCTGGTGCAGGAAATGGTGTCACTTCTTAAAGCTA 782
Db 721 ACTGTGTAACTTACCTTCTGCTGGTGCAGGAAATGGTGTCACTTCTTAAAGCTA 780

QY 783 CTGAACTTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
Db 781 CTCGAACCTTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
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QY 843 ATGAATGATATAAACTGGATGCAGTGTGTTTTCAGAAAGAGCTCATTCCAGGTTTCACTCT 902
Db 841 ATGAATGATATAAACTGGATGCAGTGTGTTTTCAGAAAGAGCTCATTCCAGGTTTCACTCT 900

QY 903 AATAAAGGCAGGCTGAATGTGATCCTACCTTGAACCTTGAGGAAATGATTTTGGAGTCC 962
Db 901 AATAAAGGCAGGCTGAATGTGATCCTACCTTGAACCTTGAGGAAATGATTTTGGAGTCC 960

QY 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAATGC 1022
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAATGC 1020

QY 1023 GATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTTATA 1082
Db 1021 GATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTTATA 1080

QY 1083 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1142
Db 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1140

QY 1143 GAACAAACCAAGACCCACAAGGTGAGGATGGTGCAGAAATAACA 1185
Db 1141 GAACAAACCAAGACCCACAAGGTGAGGATGGTGCAGAAATAACA 1183
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RESULT 6

US-09-841-683-6
; Sequence 6, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 711
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-6

Query Match 44.2%; Score 656.2; DB 4; Length 711;
Best Local Similarity 99.5%; Pred. No. 3.5e-197;
Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 3 ATGGAGCGAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGAGCGAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60

QY 63 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTGTGTTGGGAGGTCTGCAATTGA 122
Db 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTGTGTTGGGAGGTCTGCAATTGA 120

QY 123 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 182
Db 121 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGTG 180

QY 183 GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATGCAGGTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATGCAGGTCTGGAGCAC 240

QY 243 CCTTCTCTGTTAAATTTGTGTTATCTTCAAGATGAGGAGGATGTTTCAATGTTGGTG 302
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Db 157 GCCATGAAGTACATGAACAAGCAGCAGTGCATCGAGCGCGAGGTCGCAACGCTCTTC 216
Qy 210 AAGGAACCTCCAGATCATGCAGGGTCTGGAGCACCCTTCTCTGGTTAATTTGTGGTATTC 269
Db 217 CGGAGCTGGAGATCCTGCAGGAGATCGAGCAGCTTCTCTGGTGAACCTCTGGTACTCC 276
Qy 270 TTCCAAGATGAGGAAGACATGTTTCATGGTGTGGACCTCTCTGGTGGAGACCTGGCT 329
Db 277 TTCCAGGACGAGGAGGACATGTTTCATGGTGTGGACCTGCTACTGGCGGGGACCTGGCG 336
Qy 330 TATCACCTGCAACAGAACGCTCCACTTCAAGGAAGAAACAGTGAAGCTCTTCATCTGTGAG 389
Db 337 TACCACCTGCAGCAGAACGTCAGTTCCTCCAGGACACGCTGAGGCTGTACATCTGCGAG 396
Qy 390 CTGGTCATGGCCCTGGACTACCTGCAGAACCCAGCGCATCATTCACAGGATATGAAGCCT 449
Db 397 ATGGCACTGGCTCTGGACTACCTGCGCGGCGAGCAGCATCATCCACAGAGATGTCAAGCCT 456
Qy 450 GACAAATATTTACTTGACGAACATGCGGACGTCACATCACAGATTTCAACATTTCTGCG 509
Db 457 GACAAATATTTCTCTGGATGAGAGAGGACATGACACACCTGACCGACTTCAACATTTGCCACC 516
Qy 510 ATGCTGCCCCAGGAGACACAGATTTACCAACCATGGCTGGCACCAGCCTTACATGGCACCT 569
Db 517 ATCATCAAGGACGGGAGCGGGCGGACGGCATTAGCAGGACCAAGCCGTACATGGCTCCG 576
Qy 570 GAGATGTTTCAAGCTC-----CAGAAAAGGAGCAGGCTATTCCTTTGCTGTTGACTGGTG 623
Db 577 GAGATCTTCCACTCTTTTGTCAAACGGCGGGGACCGGCTACTCTCTCGAGGTGGACTGGTG 636
Qy 624 TCCCTGGGAGTGACGGCATATGAATGCTGTGAGAGCGCGGAGACCGGTATCATATTCGCTCC 683
Db 637 TCGGTGGGGGTGATGGCCCTATGAGCTGTGCGAGGATGGAGGCCCTATGACATCCACTCC 696
Qy 684 AGTACTTCCAGCAAGGAATTTGTACACACGTTTGTGAGACGACTGTTGTAACCTTACCTTCT 743
Db 697 AGCAACGCCGTGGAGTCCCTGTTGTCAGCTGTTTGTGAGCAGCTGTTGAGCAGCTGTTGAG 756
Qy 744 GCCTGGTCAACAGGAATGGTGTCACTTCTTAAAGAGCTACTCGAACCTTAATCCAGACCAA 803
Db 757 ACGTGTCCAAAGGAGATGGTGGCTTGTGCGGAAGCTCCTCACTGTGAACCCCGAGCAC 816
Qy 804 CGATTTTCTCAGTTATCTGATGTCCAGAACTTCTCCGATATGAATGATATATAAAGCTGGAT 863
Db 817 CGGCTCTCCAGCCTCCAGGACGTGCAGGACGCGCGGCTGGCGCGGCTGCTGTGGGAC 876
Qy 864 GCAGTTTCTCAGAAAGGCTCATTTCCAGGTTTCACTTCTTAATAAAGGAGGCTGAATTGT 923
Db 877 CACCTGAGCGGAGAGAGGGGTGGAGCCGGGCTTCTGTCGCCCAACAAAGGCCGTCTGCACTGC 936
Qy 924 GATCCTACTTTTGAACCTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAA 983
Db 937 GACCCCACTTTGAGCTGGAGGAGATGATCTCGAGTCCAGGCCCTTGCAAGGAAGAG 996
Qy 984 AAGCGTCTGGCAAGAGAGGA-----GAAGGATATGAGGAATGCGAATCTTCTCAGACA 1037
Db 997 AAGCGTCTGGCCAGAACAAAGTCCCGGGACAAACAGCAGGAGCAGCTCCAGTCCGAGNAT 1056
Qy 1038 TGTCTTCTCAAGAGCAGCCTTGACTCTGTCCAGAGGAGTTTCAATAATTTTCAACAGAGAA 1097
Db 1057 GACTATCTTCAAGACTGCTCGATGCCATCCAGCAAGACTTGTGATTTTAAACAGAGAA 1116
Qy 1098 AAAGTAAACAGG 1109
Db 1117 AAGCTGAAGAGG 1128

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RESULT 9

US-09-799-875-13
; Sequence 13, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:

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; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)...(1273)
US-09-799-875-13

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Query Match 32.4%; Score 481.6; DB 4; Length 1826;
Best Local Similarity 66.5%; Pred. No. 1.2e-141;
Matches 726; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

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Qy 30 CCAGTGTGATGAAATGAAGATGTCAACTTTGACCACCTTTGAAATTTTGGAGCCATT 89
Db 53 CCGGTGTTGACGACAAGGAGGACGTGAACCTTCGACCACTTCAGATCTTGGGCCATT 112
Qy 90 GGGAAAGGCGAGTTTGGGAGGCTCTGCATTTGTACAGAAATGATACCAAGAAAGATGTGC 149
Db 113 GGGAAAGGCGAGCTTTGGCAAGGTGTGCATTTGTACAGAAAGCGGAGACCGGAGAAATGTAC 172
Qy 150 GCAATGAAGTACATGAATAAAACAAAGTGCCTGGAGCGCAATGAAGTGAAGAAATGTCTTC 209
Db 173 GCCATGAAGTACATGAACAAGCAGCAGTGCATCGAGCGCGAGAGTCCGCAACGCTCTTC 232
Qy 210 AAGGAACTCCAGATCATGCAGGCTCTGGAGCACCTTTCTCTGGTTAATTTGTGGTATTC 269
Db 233 CGGAGCTGGAGATCCTGCAGGAGATCGAGCAGCTCTCTCTGGTGAACCTCTGGTACTCC 292
Qy 270 TTCCAAGATGAGGAAGACATGTTTCATGGTGGTGACCTCTCTGGTGGAGACCTGGCGT 329
Db 293 TTCCAGGACGAGGAGGACATGTTTCATGGTGGAGCTTCTGCTACTTGGCGGGGACCTGGCG 352
Qy 330 TATCACTCTGCAACAGAACGCTCCACTTCAAGGAAGAAACAGTGAAGCTTTCATCTGTGAG 389
Db 353 TACCACCTTCAGCAGAACGTCAGTTCCTCCAGGACACCGTGAAGCTGTACATCTGCGAG 412
Qy 390 CTGGTCATGGCCCTGGACTACCTGCAGAACCCAGCGCATCATTCACAGGATATGAAGCCT 449
Db 413 ATGGCACTGGCTCTGGACTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCT 472
Qy 450 GACAAATATTTACTTGACGAACATGGGACGTCGACATCACAGATTTCAACATTTGCTGCG 509
Db 473 GACAAATATTTCTCTGGATGAGAGGAGACATGCACACCTTGACCGACTTCAACATTTGCCACC 532
Qy 510 ATGCTGCCAGGAGACACAGATTTACCAACCATGGCTGGCACCAGCCTTACATGGCACCT 569
Db 533 ATCATCAAGGACGGGAGCGGGCGGCGGATAGCAGGACCAAGCCGTACATGGCTCCG 592
Qy 570 GAGATGTTTCAAGCTC-----CAGAAAAGGAGCAGGCTATTCCTTTGCTGTTGACTGGTG 623
Db 593 GAGATCTTCCACTCTTTTGTCAAACGGCGGGGACCGGCTACTCTCTCGAGGTGGACTGGTG 652
Qy 624 TCCCTGGGAGTGACGGCATATGAATGCTGTGAGAGCGCGGAGACCGGTATCATATTCGCTCC 683
Db 653 TCGGTGGGGGTGATGGCTATGAGCTGTGCTGCGAGGATGGAGGCCCTTATGACATCCACTCC 712
Qy 684 AGTACTTCCAGCAAGGAATTTGTACACGTTTGTGAGACGACTGTTGTAACCTTACCTTCT 743

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Db 713 AGCAACCGGTGGAGTCCCTGGTGCAGCTGTTTTCAGCACCGTGAGCGTCCAGTATGTCCCC 772
Qy 744 GCCTGTGCACAGGAATGGTGTCACTTCTTAAAGAGCTACTCGAACCTAATCCAGACCAA 803
Db 773 ACGTGTCCAAGGAGATGGTGGCTTGTCTGCGGAAGCTCTCACTGTGAACCCCGAGCAC 832
Qy 804 CGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTATATGATATATAAAGTGGAT 863
Db 833 CGGCTCTCAGCCTCCAGGACGTGCAGGCAGCCCGCGCTGGCGCGTCTGTGGAC 892
Qy 864 GCAGTTTTCAGAGAGGCTCATTCAGGTTTTCATTCCTTAATAAAGCGAGCTGATTGT 923
Db 893 CACCTGAGGAGAGAGGGTGGAGCGGGCTTGTGCCCCAACAAGGCGTCTGCACTGC 952
Qy 924 GATCCTACCTTTGAACCTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAA 983
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Qy 1098 AAGTAAACAGG 1109
Db 1133 AAGCTGAAGAGG 1144

RESULT 10

US-09-819-607-1
; Sequence 1, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Human
US-09-819-607-1

Query Match 31.4%; Score 466.8; DB 4; Length 1864;
Best Local Similarity 65.9%; Pred. No. 5.9e-137;
Matches 713; Conservative 0; Mismatches 357; Indels 12; Gaps 2;

Qy 40 ATGAAATGAAGATGTCAACTTTGACCACTTTGAAATTTTGGAGCCATTTGGGAAGGCA 99
Db 89 AAGCAGAGAGGAGTGAAGTTCGACCACTTCCAGATCTTCCGGCCATTTGGGAAGGCA 148
Qy 100 GTTTTGGGGAGTGTGATTTGTACAGAGAGATGATACCAAGAGATGTGCGCAATGAAGT 159
Db 149 GCTTTGGCAAGTGTGATTTGTGAGAGAGCGGACACGGAGAGATGTACGCCATGAAGT 208
Qy 160 ACATGAATAACAAGAGTGGTGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAATCC 219
Db 209 ACATGAACAAGCAGCAGTGCATCGAGCGGACAGGAGTCCGCAACGTCTCCGGAGCTGG 268
Qy 220 AGATCATGAGGCTGTGGAGCACCTTTCTGGTTAATTTGTGGTATTCCTTCCAAGATG 279
Db 269 AGATCCTGCAGGAGATCGAGCACGCTTCTCGGTGAACCTCTGGTACTCTTCCAGGACG 328
Qy 280 AGGAAGACATGTTTCATGGTGGTGGACCTCTGCTGGTGGAGACCTGCGTTATCACCTGC 339

RESULT 11

US-09-801-876B-3
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0

Db 329 AGGAGGACATGTTTCATGGTCTGTGGACCTGCTACTGGGGGGGACCTGCGCTACCACCTGC 388
Qy 340 AACAGAACGTCCTCACTTCAAGGAAGAAACAGTGAAGCTCTTTCATCTGTAGCTGTGTCATGG 399
Db 389 AGCAGAACGTCGAGTTCCTCGAGGACACGGTGAAGCTGTACATCTCGAGATGGCACTGG 448
Qy 400 CCCTGGACTACCTGSCAGAACCCAGCGCATCATTCACAGGGATATGAAGCCTGACAAATATT 459
Db 449 CTCTGGACTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAAATTC 508
Qy 460 TACTTGACGAACATGGGCACGTGCACATCACAGATTTCAACATTTGCTGCGATGTGCCCCA 519
Db 509 TCCTGGATGAGAGAGGACATGCACACCTGACCGACTTCAACATTTGCCACCATCATCAAGG 568
Qy 520 GGGAGACACAGATTACCAACCATGGCTGGCACCAGCCCTTACATGGCACCTGAGATGTTCA 579
Db 569 ACGGGAGCGGGCGAGCGCATTAGCAGGCACCCAGCCGTACATGGCTCCGAGATCTTCC 628
Qy 580 GCTC-----CAGAAAGGAGCAGGCTATTCTTTGCTGTGTGACTGGTGGTCCCTGGGAG 633
Db 629 ACTCTTTTGTCAACGCGGGGACCGGCTACTCTCTGAGGTGGACTGGTGGTGGTGGGG 688
Qy 634 TGACGGCATATGAACCTGTGAGAGCGCGGAGACCGTATCATATTGCTCCAGTACTTCCA 693
Db 689 TGATGGCCTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCG 748
Qy 694 GCAAGGAATTTGTACACACGTTTGTGAGACGACTGTTGTAACTTACCCCTTCTGCTGTGTAC 753
Db 749 TGGAGTCCCTGGTGCAGCTGTTTTCAGCACCGTGCAGCTCCAGTATGTCCCCACGTTGCCA 808
Qy 754 AGGAATGGTGTCACTTCTTAAAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTC 813
Db 809 AGGAGATGGTGGCTTGTGCGGAAGCTCTCTCACTGTGAACCCCGAGCACCGGCTTCCA 868
Qy 814 AGTTATCTGATGTCAGAACTTCCCGTATATGATATATAAAGTGGATGCGATTTTTC 873
Db 869 GCCTCCAGGACGTGCAGGACGCCCCCGGCGTGGCGCGGTGCTGTGGGACCACTGAGCG 928
Qy 874 AGAAGAGGCTCATTCAGGTTTTCATTCCTTAATAAGGCGAGGCTGAATTTGTGATCTTACCT 933
Db 929 AGAAGAGGTTGGAGCGGGCTTCTGTGCCCCAACAAAGGCGCTGTGCACTGCGACCCACCT 988
Qy 934 TTGAACCTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAAGCGTCTGG 993
Db 989 TTGAGCTGGAGGAGATGATCTTGGAGTCCAGGCCCTGCAAGAGAGAGAGAGCGCTGG 1048
Qy 994 CAAAGAAGGA-----GAAGGATATGAGGAATGCGAATTCCTTCTCAGACATGTCTTCTTC 1047
Db 1049 CCAAGAACAAGTCCCGGACAAACAGCAGGAGGACAGCTCCAGTCCGAGATGACTATCTTC 1108
Qy 1048 AAGAGCACCTTGACTCTGTCCAGAGGAGTTTCAATAATTTTCAACAGAGAAAAAGTAAACA 1107
Db 1109 AAGACTGCTCGATGCCATCCAGCAAGACTTCTGATGATTTTAAACAGAGAAAAAGCTGAAGA 1168
Qy 1108 GG 1109
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QY 294 ATGGTGGTGGACCTCTCTGGTGGGAGACCTGCTTATCACCTGCAACAGAACGTCCAC 353
Db 310 ATGGTCATGGAGTACGTGCGCGGGGAGATGTTCTCACACCTACGGCGGATCGAAGG 369
QY 354 TTCAAGGAAGAAACAGTGAAGCTCTTCTATCTGTGAGCTGGTCAATGCTGCTGACTACCTG 413
Db 370 TTCAAGTGAACCCCATGCGCTTCTACGCGGCCAGATGCTCTGACCTTTGAGTATCTG 429
QY 414 CAGAACCCAGCGCATCTTACAGGGGATATGAAGCCTGACAAATATTTTACTTGACGAACAT 473
Db 430 CACTCGCTGGATCTCATCTACAGGGACCTGAAGCCGGAGAACTGTCTCATTTGACCAGCAG 489
QY 474 GGGCACGTGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATT 533
Db 490 GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----GCGGTGAAGGGCCGCACT 543
QY 534 ACCACCATGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGA 593
Db 544 TGGACCTTGTGCGGCACCCCTGAGTACCTGGCCCTGAGATTATCTCTATGAATG 651
QY 594 GCAGGCTATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAAGT 650
Db 597 --AGGCTACAACAAGGCCGTGACTGGTGGCCCTGGGGCTTCTTATCTATGAATG 776

RESULT 14

US-09-467-082-3

; Sequence 3, Application US/09467082

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION

; FILE REFERENCE: RTS-0088

; CURRENT FILING DATE: 1999-12-17

; NUMBER OF SEQ ID NOS: 49

; SEQ ID NO 3

; LENGTH: 2549

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (81)..(1136)

; NAME/KEY: unsure

; LOCATION: 6

; OTHER INFORMATION: unknown

US-09-467-082-3

Query Match 8.9%; Score 132.6; DB 3; Length 2549;
Best Local Similarity 54.1%; Pred. No. 4e-31;
Matches 323; Conservative 0; Mismatches 259; Indels 15; Gaps 2;

QY 54 GTCAACTTTGACCACCTTTGAAATTTTGGAGCCATTGGGAAGGCAGTTTTGGGGAGGTC 113
Db 195 GCCCACTTGGATCAGTTTGAACGAATCAAGACCCCTCGGCACGGGCTCCTTCGGGCGGCTG 254
QY 114 TGCATTGTACAGAAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAA 173
Db 255 ATGCTGGTGAACACCAAGGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAACAG 314
QY 174 AAGTGGTGGAGCGCAATGAAGTGAAGAAATGTTTCAAGGAATCCAGATCATGCGGCT 233
Db 315 AAGGTGGTGAACACTGAACAGATCGAACACACCCCTGAATGAAGAAGCGCATCCTGCAAGCT 374
QY 234 CTGGAGCACCTTTCTGTTTAAATTTGTGGTATTCCTTCCAGATGAGGAAGACATGTTTC 293
Db 375 GTCAACTTTCCGTTCTCGTCAAACTCGAGTTCCTTCAAGGACAACTCAAACTTATAC 434
QY 294 ATGGTGGTGGACCTCTCTGCTGGTGGAGACCTGCGTTATCATCTGCAACAGAACGTCCAC 353
Db 435 ATGGTCATGGAGTACGTGCCCGGGGAGATGTTCTCACACCTACGGCGGATCGGAAGG 494
QY 354 TTCAAGGAAGAAACAGTGAAGCTTCTTATCTGTGAGCTGGTCTATGGCCCTGGACTACCTG 413

Db 495 TTCAGTGAGCCCCCATGCCCCGTTTCTACGGGGCCAGATCGTCTGACCTTTGAGTATCTG 554
QY 414 CAGAACCCAGCGCATCATTCACAGGATATGAAGCCTGACAATATTTTACTTGACGAACAT 473
Db 555 CACTCGCTGGATCTCATCTACAGGACCTGAAGCCGGAGAACTGCTCATTTGACCAGCAG 614
QY 474 GGGCACGTGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATT 533
Db 615 GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----GCGGTGAAGGGCCGCACT 668
QY 534 ACCACCATGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGA 593
Db 669 TGGACCTTGTGCGGCACCCCTGAGTACCTGGCCCTGAGATTATCTCTGAGCAA----- 721
QY 594 GCAGGCTATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAAGT 650
Db 722 --AGGCTACAACAAGGCCGTGACTGGTGGCCCTGGGGCTTCTTATCTATGAATG 776

RESULT 15

US-09-394-455-5

; Sequence 5, Application US/09394455

; Patent No. 6531305

; GENERAL INFORMATION:

; APPLICANT: Witman, George F.

; APPLICANT: San Agustín, Jovenal

; APPLICANT: Leszyk, John D.

; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING

; FILE REFERENCE: 07917/078001

; CURRENT FILING DATE: 1999-09-10

; PRIOR FILING DATE: 1998-09-10

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 2549

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (81)..(1133)

; NAME/KEY: misc_feature

; LOCATION: (1)..(2549)

; OTHER INFORMATION: n = A, T, C or G

US-09-394-455-5

Query Match 8.9%; Score 132.6; DB 4; Length 2549;
Best Local Similarity 54.1%; Pred. No. 4e-31;
Matches 323; Conservative 0; Mismatches 259; Indels 15; Gaps 2;

QY 54 GTCAACTTTGACCACCTTTGAAATTTTGGAGCCATTGGGAAGGCAGTTTTGGGGAGGTC 113
Db 195 GCCCACTTGGATCAGTTTGAACGAATCAAGACCCCTCGGCACGGGCTCCTTCGGGCGGCTG 254
QY 114 TGCATTGTACAGAAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAA 173
Db 255 ATGCTGGTGAACACCAAGGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAACAG 314
QY 174 AAGTGGTGGAGCGCAATGAAGTGAAGAAATGTTTCAAGGAATCCAGATCATGCGGCT 233
Db 315 AAGGTGGTGAACACTGAACAGATCGAACACACCCCTGAATGAAGAAGCGCATCCTGCAAGCT 374
QY 234 CTGGAGCACCTTTCTGTTTAAATTTGTGGTATTCCTTCCAGATGAGGAAGACATGTTTC 293
Db 375 GTCAACTTTCCGTTCTCGTCAAACTCGAGTTCCTTCAAGGACAACTCAAACTTATAC 434
QY 294 ATGGTGGTGGACCTCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCAC 353
Db 435 ATGGTCATGGAGTACGTGCCCGGGGAGATGTTCTCACACCTACGGCGGATCGGAAGG 494

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:01:41 ; Search time 467 Seconds
(without alignments)
13508.724 Million cell updates/sec

Title: US-10-667-442-1
Perfect score: 1485
Sequence: 1 ccacggagcgcaacacttca.....taaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:  geneseqn1990s: *
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10: geneseqn2004s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match					
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2	1485	100.0	1485	8	ACA62840	ACA62840	cdNA enco
3	1228.6	82.7	1281	6	AAI170704	AAI170704	Human 149
4	1188.2	80.0	1594	4	AAH46891	AaH46891	cdNA enco
5	1188.2	80.0	1594	6	AAD34317	Aad34317	Human PKI
6	1186.2	79.9	1191	6	AAD23679	Aad23679	Novel hum
7	1162.6	78.3	1675	6	AAD23680	Aad23680	Novel hum
8	1160.6	78.2	1224	6	AAD23678	Aad23678	Novel hum
9	831.2	56.0	981	4	AAS06704	Aas06704	Polynucle
10	672.8	45.3	678	4	ABA08463	Aba08463	Human Ser
11	656.2	44.2	711	6	AAD23677	Aad23677	Novel hum
12	655.2	44.1	678	6	AAD23676	Aad23676	Novel hum
13	540.8	36.4	1587	6	ABQ61051	AbQ61051	Serine/th
14	540.8	36.4	3224	4	AAF44625	Aaf44625	Novel pro
15	540.8	36.4	3224	7	ADA19317	Ada19317	Human ins
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18	516.4	34.8	3244	4	AAS46210	Aas46210	Human DNA
19	516.4	34.8	3244	7	ABX78813	Abx78813	Human PRO
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23	516.4	34.8	3244	7	ACC87179	Acc87179	Human sec

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27	516.4	34.8	3244	7	ACC89635	Acc89635	Human sec
28	516.4	34.8	3244	7	ACA98426	Aca98426	Novel hum
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39	516.4	34.8	3244	7	ACA73670	Aca73670	Human sec
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ALIGNMENTS

RESULT 1

ABS55499

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1000

AC
ABS55499;

XX DT 14-JAN-2003 (first entry)

DI
XX
14-00000-2003 (1118C encry)

DE cDNA encoding human serine

XXXXXXXXXXXXXXXXXXXX

KW Human; kinase; serine/thre

gene therapy; chromosome 5

800-762-2264

US
xx
Homo sapiens.

XX	Key	Location/Comments
EH		

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3. U.R.

Page 11 of 11

PN US2002127683-A1.

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PD 12-SEP-2002.

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PF 09-MAR-2001; 2001US-008018

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09-MAR-2001: 200111S-008019

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QY 1261 CTGACAGTAGCTCCTGCCACTCCACACACCATGACTTAGAAAATGTGAATGAATATATT 1320
Db 1261 CTGACAGTAGCTCCTGCCACTCCACACACCATGACTTAGAAAATGTGAATGAATATATT 1320
QY 1321 CAAAAAGGCAGCAGCAACACAGTGAAGGGTCTGGGCTGAGCTCCTGGAAAGTCATTTC 1380
Db 1321 CAAAAAGGCAGCAGCAACACAGTGAAGGGTCTGGGCTGAGCTCCTGGAAAGTCATTTC 1380
QY 1381 ACATCAATCAACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTACTTTA 1440
Db 1381 ACATCAATCAACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTACTTTA 1440
QY 1441 TTTATCTAAATGAGAGGGTTATATAAAAAA 1485
Db 1441 TTTATCTAAATGAGAGGGTTATATAAAAAA 1485

RESULT 3

AAI70704
ID AAI70704 standard; cDNA; 1281 BP.
XX AAI70704;
AC AAI70704;
XX AAI70704;
DT 04-FEB-2002 (first entry)
XX Human 14911 protein kinase cDNA.
DE Protein kinase; human; signal transduction; lung cancer; colon cancer;
KW brain cancer; breast cancer; gene therapy; diagnosis; ss.
XX Homo sapiens.
OS
XX
FH Key
FT CDS
FT 49.1239
FT /*tag= a
XX
PN WO200181589-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013785.
XX
PR 25-APR-2000; 2000US-0199391P.
PR 15-JUN-2000; 2000US-00593927.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R, Hunter JJ;
XX
DR WPI; 2002-041408/05.
DR P-PSDB; AAM50334.
XX
PT Novel protein kinase nucleic acid molecules and the encoded proteins for
PT diagnosing and treating cellular proliferative, bone, immune,
PT cardiovascular, liver, pain or metabolic disorders and identifying
PT modulators.
XX
PS Claim 1(a); Fig 1A-B; 115pp; English.
XX
CC The present cDNA sequence, the coding region of which is also claimed,
CC encodes a novel human protein kinase, designated 14911 (see AAM50334).
CC This protein kinase plays a role in, or functions in, the transduction of
CC signals for cell proliferation, differentiation and apoptosis, modulating
CC the activity of one or more proteins involved in cellular growth or
CC differentiation. 14911 molecules are overexpressed in some tumour cells,
CC where they may inappropriately propagate either cell proliferation or
CC cell survival signals. The invention provides methods for the diagnosis
CC and treatment of cancer, including breast colon, brain and especially

CC lung cancer (claimed), and methods for evaluating the efficacy of
CC treatment. 14911 nucleic acids are useful in diagnostic, screening and
CC gene therapy methods, for recombinant protein production, in the design
CC of probes and primers, as a pharmacogenomics marker, and in the breeding
CC of transgenic animals in which a 14911 gene is introduced or disrupted.
CC Antisense 14911 and ribozyme molecules are used in a claimed method of
CC treating cancer or a cellular proliferation and/or differentiation
CC disorder. In addition to cancer, such disorders include those associated
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,
CC liver disorders, viral diseases, pain and metabolic disorders
XX
SQ Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;

Query Match 82.7%; Score 1228.6; DB 6; Length 1281;
Best local Similarity 99.7%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCATGGGAGCGCAACACTTCAAGAAAACCAACCACTGTTTGTATGAATAATGAAGATGTCAACT 60
Db 47 CCATGGGAGCGCAACACTTCAAGAAAACCAACCACTGTTTGTATGAATAATGAAGATGTCAACT 106
QY 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGGAGGCTCTGCATTG 120
Db 107 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAAGGCTCTGCATTG 166
QY 121 TACAGAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
Db 167 TACAGAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 226
QY 181 TGGAGCGCAATGAAGTGAATAATGTTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGC 240
Db 227 TGGAGCGCAATGAAGTGAATAATGTTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGC 286
QY 241 ACCCTTCTCTGGTTAATTTGTGTATTTCTTCAAGATGAGGAAGACATGTTTCAATGGTGG 300
Db 287 ACCCTTCTCTGGTTAATTTGTGTATTTCTTCAAGATGAGGAAGACATGTTTCAATGGTGG 346
QY 301 TGGACCTCTCTGGTGGAGACCTTGGTTATCACCTGCAACAGAACGTCACCTTCAAGG 360
Db 347 TGGACCTCTCTGGTGGAGACCTTGGTTATCACCTGCAACAGAACGTCACCTTCAAGG 406
QY 361 AAGAAACAGTGAAGCTCTTCACTCTGTGAGCTGGTCACTGGCCCTGGACTACCTGCAGAAC 420
Db 407 AAGAAACAGTGAAGCTCTTCACTCTGTGAGCTGGTCACTGGCCCTGGACTACCTGCAGAAC 466
QY 421 AGCGCATATTACAGGGATATGAAGCTGACAAATATTTTACTTGACGAACATGGGCACG 480
Db 467 AGCGCATATTACAGGGATATGAAGCTGACAAATATTTTACTTGACGAACATGGGCACG 526
QY 481 TGCACATCAGAGATTTCAACATTTGTGCGATGCTGCCAGGGAGACACAGATTACCACCA 540
Db 527 TGCACATCAGAGATTTCAACATTTGTGCGATGCTGCCAGGGAGATACAGATTACCACCA 586
QY 541 TGGCTGGCAACCAAGCCTTACATGGCACTGAGATGTTTCACTCCAGAAAAGGAGCAGGCT 600
Db 587 TGGCTGGCAACCAAGCCTTACATGGCACTGAGATGTTTCACTCCAGAAAAGGAGCAGGCT 646
QY 601 ATTCTTTTGTGTTGACTGGTGTCTCCCTGGGAGTGACGGCATATGAAGTGTGAGAGGCC 660
Db 647 ATTCTTTTGTGTTGACTGGTGTCTCCCTGGGAGTGACGGCATATGAAGTGTGAGAGGCC 706
QY 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTGAGA 720
Db 707 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTGAGA 766
QY 721 CGACTGTTGTAACCTTACCTTCTGCTGGTCAAGGAAATGTTGTTTCTTAAAAAGC 780
Db 767 CGACTGTTGTAACCTTACCTTCTGCTGGTCAAGGAAATGTTGTTTCTTAAAAAGC 826
QY 781 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Db 827 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 886

QY 841 ATATGATGATATAAACTGGGATGCGAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTC 900
Db |||||||
QY 887 ATATGATGATATAAACTGGGATGCGAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTC 946
Db |||||||
QY 901 CTAATAAGGAGGCTGAATTTGATCCTTACCTTTGAACCTTGAGGAATGATTTTGGAGT 960
Db |||||||
QY 947 CTAATAAGGAGGCTGAATTTGATCCTTACCTTTGAACCTTGAGGAATGATTTTGGAGT 1006
Db |||||||
QY 961 CCAAACTCTACATAAAGAAAAAAGCGCTGCGCAAGAGGAGGAGGATATGAGGAAT 1020
Db |||||||
QY 1007 CCAAACTCTACATAAAGAAAAAAGCGCTGCGCAAGAGGAGGAGGATATGAGGAAT 1066
Db |||||||
QY 1021 GCGATTCTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGCTCCAGAGGAGTTCA 1080
Db |||||||
QY 1067 GCGATTCTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGCTCCAGAGGAGTTCA 1126
Db |||||||
QY 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAACTAGCCT 1140
Db |||||||
QY 1127 TAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAACTAGCCT 1186
Db |||||||
QY 1141 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAGAATAACAACTTGTAAAGGCCTC 1200
Db |||||||
QY 1187 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAGAATAACAACTTGTAAAGGCCTC 1246
Db |||||||
QY 1201 ATGTCTTCTTCTTGGGACAAATCTCATGCCAGAAAC 1235
Db |||||||
QY 1247 ATGTCTTCTTCTTGGGACAAATCTCATGCCAGAAAC 1281
Db |||||||

RESULT 4

AAH46891
ID AAH46891 standard; cDNA; 1594 BP.

AC AAH46891;
XX

DT 25-SEP-2001 (first entry)

DE cDNA encoding human protein kinase SGK177.

XX
KW protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
KW antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic;
KW osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;
KW vasotrophic; antidiabetic; gene therapy; ss.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 404..1594
FT /*tag= a

XX WO200155356-A2.

PN 02-AUG-2001.

PD 25-JAN-2001; 2001WO-US002337.

PR 25-JAN-2000; 2000US-0178078P.

PR 31-JAN-2000; 2000US-0179364P.

PR 17-FEB-2000; 2000US-0183173P.

PR 17-MAR-2000; 2000US-0190162P.

PR 29-MAR-2000; 2000US-0193404P.

PR 13-NOV-2000; 2000US-0247013P.

XX (SUGE-) SUGEN INC.

PA Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI WPI; 2001-476202/51.

DR P-PSDB; AAB85491.

XX Kinase polypeptides useful for treating cancers, Alzheimer's disease,

PT

PT viral infections, diabetes, obesity, organ transplant rejection and
PT rheumatoid arthritis.

XX
PS Example 1; Page 201; 218pp; English.

XX
CC The invention provides human protein kinases and protein kinase-like
CC enzymes and polynucleotides encoding the polypeptides. The kinase
CC polypeptides and their modulators are useful for treating a disease or
CC disorder such as cancer, immune-related diseases, cardiovascular disease,
CC brain or neuronal-associated disease and metabolic disorders, including
CC cancers of tissues, cancers of hematopoietic origin, diseases of the
CC central nervous system, diseases of the peripheral nervous system,
CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
CC lateral sclerosis, viral infections, infections caused by prions,
CC bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
CC mood disorders, attention disorders, cognitive disorders, hypotension,
CC hypertension, psychotic disorders, neurological disorders, dyskinesias,
CC metabolic disorders, and organ transplant rejection. They are also useful
CC for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
CC osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
CC inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
CC such as diabetes, obesity, cardiovascular diseases such as reperfusion
CC injury, coronary thrombosis, clotting disorders and atherosclerosis,
CC ocular diseases such as glaucoma, retinopathy and macular degeneration,
CC psychiatric and neurological disorders such as anxiety, schizophrenia,
CC dementia, manic depression, etc. The polynucleotides are useful in gene
CC therapy techniques to treat the above mentioned disorders. Sequences
CC AAH46891-46922 represent human protein kinases encoding cDNA molecules
XX

SQ Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;

Query Match 80.0%; Score 1188.2; DB 4; Length 1594;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGGGAGCGAACACTTCAAGAAAAACCCACAGTGTGTTGATGAAAAATGAAGATGTCAACT 60
Db |||||||
QY 402 CCATGGGAGCGAACACTTCAAGAAAAACCCACAGTGTGTTGATGAAAAATGAAGATGTCAACT 461
Db |||||||
QY 61 TTGACCACCTTTGAAATTTTGGAGGCCATTTGGGAAAGCGAGTTTGGGGAGGCTGTGATTG 120
Db |||||||
QY 462 TTGACCACCTTTGAAATTTTGGAGGCCATTTGGGAAAGCGAGTTTGGGGAGGCTGTGATTG 521
Db |||||||
QY 121 TACAGAAGAATGATACCAAGAGAGATGTGCGCAATGAAGTACATGAATAACAAAGTGGC 180
Db |||||||
QY 522 TACAGAAGAATGATACCAAGAGAGATGTGCGCAATGAAGTACATGAATAACAAAGTGGC 581
Db |||||||
QY 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGC 240
Db |||||||
QY 582 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGCAGGCTCTGGAGC 641
Db |||||||
QY 241 ACCCTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTG 300
Db |||||||
QY 642 ACCCTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTG 701
Db |||||||
QY 301 TGGACCTCTGCTGGTGGAGACCTGCGTTATTCACCTGCAACAGAAACGTCCACTTCAAGG 360
Db |||||||
QY 702 TGGACCTCTGCTGGTGGAGACCTGCGTTATTCACCTGCAACAGAAACGTCCACTTCAAGG 761
Db |||||||
QY 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 420
Db |||||||
QY 762 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 821
Db |||||||
QY 421 AGCGCATATTCAAGGAGATGAAGCCTGCAATATTTTACTTTGACGAACATGGGCACG 480
Db |||||||
QY 822 AGCGCATATTCAAGGAGATGAAGCCTGCAATATTTTACTTTGACGAACATGGGCACG 881
Db |||||||
QY 481 TGCACATCACAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTACCACCA 540
Db |||||||
QY 882 TGCACATCACAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTACCACCA 941
Db |||||||
QY 541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCT 600
Db |||||||

Db 942 TGGCTGGCACCAAGCCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCT 1001
Qy 601 ATTCTTTGCTGTTGACTGGTCCCTGGGAGTGACGGCATATGAACGTCTGAGAGGCC 660
Db 1002 ATTCTTTGCTGTTGACTGGTCCCTGGGAGTGACGGCATATGAACGTCTGAGAGGCC 1061
Qy 661 GGAGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 720
Db 1062 GGAGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGA 1121
Qy 721 CGACTGTTGTAACCTTACCTTCTGCTGGTGCACAGGAATGGTGTCACTTCTTAAAAAGC 780
Db 1122 CGACTGTTGTAACCTTACCTTCTGCTGGTGCACAGGAATGGTGTCACTTCTTAAAAAGC 1181
Qy 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Db 1182 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 1241
Qy 841 ATATGAATGATATAAACTGGGATGAGTGTGTTTTCAGAAAGGCTCATTCAGGTTTCAATC 900
Db 1242 ATATGAATGATATAAACTGGGATGAGTGTGTTTTCAGAAAGGCTCATTCAGGTTTCAATC 1301
Qy 901 CTAATAAAGGCAGGCTGAATTTGTGATCTCTTGAACCTTGAAGAAATGATTTTGGAGT 960
Db 1302 CTAATAAAGGCAGGCTGAATTTGTGATCTCTTGAACCTTGAAGAAATGATTTTGGAGT 1361
Qy 961 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1020
Db 1362 CCAAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1421
Qy 1021 GCGATTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTCA 1080
Db 1422 GCGATTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTCA 1481
Qy 1081 TAAATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGAACCAACCAATCTAGCCT 1140
Db 1482 TAAATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGAACCAACCAATCTAGCCT 1541
Qy 1141 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAGAAATACAACTTGTA 1193
Db 1542 TGGAAACAAACCAAGACCCCAAGGTGAGGATGGTCAGAAATACAACTTGTA 1594

RESULT 5
AAD34317
ID AAD34317 standard; cDNA; 1594 BP.

XX AAD34317;

DT 16-JUL-2002 (first entry)

DE Human PKIN-20 cDNA.

XX Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia;
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;
KW Down's syndrome; gene therapy; protein therapy; cytostatic; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 404..1594

FT /*tag= a

FT /product= "Human PKIN-20 protein"

XX WO200218557-A2.

PD 07-MAR-2002.

XX 31-AUG-2001; 2001WO-US027219.

XX

PR 31-AUG-2000; 2000US-0229873P.
PR 08-SEP-2000; 2000US-0231357P.
PR 14-SEP-2000; 2000US-0232654P.
PR 22-SEP-2000; 2000US-0234902P.
PR 29-SEP-2000; 2000US-0236499P.
PR 06-OCT-2000; 2000US-0238389P.
PR 13-OCT-2000; 2000US-0240542P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX

PI Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
PI Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
PI Burford N;
XX

DR WPI; 2002-329769/36.
DR P-PSDB; AAE21725.

PT New human kinases, useful for diagnosing, treating or preventing immune
PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
PT epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
PT or lymphoma).
XX

PS Claim 99; Page 214; 218pp; English.

XX The present invention relates to human kinases (PKIN) and polynucleotides
CC encoding such proteins. PKIN sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of PKIN, particularly immune system disorders (e.g. acquired
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma),
CC and developmental disorders (e.g. Down's syndrome). They are also used in
CC gene therapy and protein therapy. The present sequence is a cDNA encoding
CC human PKIN-20 protein
XX

SQ Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;

Query Match 80.0%; Score 1188.2; DB 6; Length 1594;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACAACCTTCAAGAAACCCAGGCTTGTGATGAAATGAAGATGTCAACT 60
Db 402 CCATGGGAGCGAACAACCTTCAAGAAACCCAGGCTTGTGATGAAATGAAGATGTCAACT 461
Qy 61 TTGACCACTTTGAAATTTTGGAGGCCATTGGGAAAGGAGGCTTGGGGAGGCTGTCATTG 120
Db 462 TTGACCACTTTGAAATTTTGGAGGCCATTGGGAAAGGAGGCTTGGGGAGGCTGTCATTG 521
Qy 121 TACAGAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
Db 522 TACAGAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 581
Qy 181 TGGAGCGCAATGAAGTGAGAATGTCTTCAAGGAACCTCCAGATCATGCAGGCTCTGGAGC 240
Db 582 TGGAGCGCAATGAAGTGAGAATGTCTTCAAGGAACCTCCAGATCATGCAGGCTCTGGAGC 641
Qy 241 ACCCTTCTCTGGTTAATTTGTGGTATTCTTCCAAAGTGAAGAGACATGTTTCATGTTGG 300
Db 642 ACCCTTCTCTGGTTAATTTGTGGTATTCTTCCAAAGTGAAGAGACATGTTTCATGTTGG 701
Qy 301 TGGACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGCTCCACITCAAGG 360
Db 702 TGGACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGCTCCACITCAAGG 761
Qy 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAAC 420
Db 762 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAAC 821

Db 361 GAAACAGTGAAGCTCTTCTATCTGTGAGCTGGTCTATGGCCCTGGACTACCTGCAGAACCCAG 420
Qy 423 CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTACTTGACGAACATGGGCACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTACTTGACGAACATGGGCACGTG 480
Qy 483 CACATCACAGATTTCACAAATGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542
Db 481 CACATCACAGATTTCACAAATGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 540
Qy 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTACAGCTCCAGAAAAGGAGCAGGCTAT 602
Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTACAGCTCCAGAAAAGGAGCAGGCTAT 600
Qy 603 TCCTTTGCTGTGACTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCCGG 662
Db 601 TCCTTTGCTGTGACTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCCGG 660
Qy 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAGACG 722
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAGACG 720
Qy 723 ACTGTTGTAACTTACCTTCTGCCTGGTCCACAGGAATGGTGTCACTTCTTAAAAAGCTA 782
Db 721 ACTGTTGTAACTTACCTTCTGCCTGGTCCACAGGAATGGTGTCACTTCTTAAAAAGCTA 780
Qy 783 CTCGAACCTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
Db 781 CTCGAACCTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Qy 843 ATGAATGATATAAATCTGGATGCGATTTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 902
Db 841 ATGAATGATATAAATCTGGATGCGATTTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 900
Qy 903 AATAAAGGCAGGCTGAATTTGTGATCCTACCTTTGAACTTGAGGAATGATTTTGAGTCC 962
Db 901 AATAAAGGCAGGCTGAATTTGTGATCCTACCTTTGAACTTGAGGAATGATTTTGAGTCC 960
Qy 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAATGC 1022
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAATGC 1020
Qy 1023 GATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCATA 1082
Db 1021 GATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCATA 1080
Qy 1083 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1142
Db 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
Qy 1143 GAACAAACCAAGACCCCAAGGTGAGGATGTTTCAGATTAACAACTTGTA 1193
Db 1141 GAACAAACCAAGACCCCAAGGTGAGGATGTTTCAGATTAACAACTTGTA 1191

RESULT 7
AAD23680
ID AAD23680 standard; DNA; 1675 BP.
XX
AC AAD23680;
XX
DT 07-MAR-2002 (first entry)
XX
DE Novel human protein (NHP) kinase full-length ORF and flanking region DNA.
XX
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic;
ds.
XX
OS Homo sapiens.
XX

PN WO200181557-A2.
XX 01-NOV-2001.
PD
XX 24-APR-2001; 2001WO-US013149.
PF
XX 25-APR-2000; 2000US-0199499P.
PR 01-MAY-2000; 2000US-0201227P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
XX WPI; 2002-034442/04.
DR
XX New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.
XX
PS Disclosure; Page 44; 44pp; English.
XX
CC The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase full-length ORF (open
CC reading frame) and flanking region DNA related to the invention
XX
SQ Sequence 1675 BP; 469 A; 404 C; 414 G; 388 T; 0 U; 0 Other;
Query Match 78.3%; Score 1162.6; DB 6; Length 1675;
Best Local Similarity 98.8%; Pred. No. 6.7e-312;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 CCATGGGAGCGCAACACTTCAAGAAAACCAACAGATGTTGATGAAAATGAAGATGTCAACT 60
Db 411 CCATGGGAGCGCAACACTTCAAGAAAACCAACAGATGTTGATGAAAATGAAGATGTCAACT 470
Qy 61 TTGACCACTTTGAAATTTTTCGAGCCATTTGGGAAAGGCAGTTTGGGAGGTCTGCATTG 120
Db 471 TTGACCACTTTGAAATTTTTCGAGCCATTTGGGAAAGGCAGTTTGGGAGGTCTGCATTG 530
Qy 121 TACAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGATGCG 180
Db 531 TACAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGATGCG 590
Qy 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCAAGGTCTGGAGC 240
Db 591 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCAAGGTCTGGAGC 650
Qy 241 ACCCTTCTCTGTTAATTTGTGTTATTTCTTCCAGATGAGGAAGACATGTTTCATGTTGG 300
Db 651 ACCCTTCTCTGTTAATTTGTGTTATTTCTTCCAGATGAGGAAGACATGTTTCATGTTGG 710
Qy 301 TGGACCTCTCTGTTGGTGGAGACCTCGGTATACCTGCAACAGAACCTTCACTTCAAGG 360
Db 711 TGGACCTCTCTGTTGGTGGAGACCTCGGTATACCTGCAACAGAACCTTCACTTCAAGG 770
Qy 361 AAGAAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACTGCAGAAC 420
Db 771 AAGAAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGGCCCTGGACTACTGCAGAAC 830
Qy 421 AGCGCATCATTCACAGGGATATGAAGCCTTGACAATATTTTACTTGACGAACATGGGCACG 480

Db 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCTATGGCCCTGGACTACCTGCAGAACCCAG 420
Qy 423 CGCATATTCACAGGGATATGAGCCTGACAAATATTTTACTTTGACGAACATGGGCACGTG 482
Db 421 CGCATATTCACAGGGATATGAGCCTGACAAATATTTTACTTTGACGAACATGGGCACGTG 480
Qy 483 CACATCACAGATTTCAACATTTGCTGGGATGCTGCCCGAGGAGACACAGATTACCAACCATG 542
Db 481 CACATCACAGATTTCAACATTTGCTGGGATGCTGCCCGAGGAGACACAGATTACCAACCATG 540
Qy 543 GCTGGACCAAGCCCTTACATGGCACCTGAGATGTTTCCAGTCCAGAAAGGAGGAGGCTAT 602
Db 541 GCTGGACCAAGCCCTTACATGGCACCTGAGATGTTTCCAGTCCAGAAAGGAGGAGGCTAT 600
Qy 603 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGCAATATGAACTGCTGAGAGCCGG 662
Db 601 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGCAATATGAACTGCTGAGAGCCGG 660
Qy 663 AGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTTCAGACG 722
Db 661 AGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTTCAGACG 720
Qy 723 ACTGTTGTAACTTACCCCTTCTGCTGGTCCAGGAAATGTTGTCACCTTCTTAAAAAGCTA 782
Db 721 ACTGTTGTAACTTACCCCTTCTGCTGGTCCAGGAAATGTTGTCACCTTCTTAAAAAGCTA 780
Qy 783 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
Db 781 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Qy 843 ATGAATGATATAAACTGGGATGCGATTTTTCAGAAAGGCTCATTCCAGGTTTTCATTCCT 902
Db 841 ATGAATGATATAAACTGGGATGCGATTTTTCAGAAAGGCTCATTCCAGGTTTTCATTCCT 900
Qy 903 AATAAAGCAGGCTGAATTTGATCTTACCTTTGAACTTGAAGTGAAGAAATGATTTTGGAGTCC 962
Db 901 AATAAAGCAGGCTGAATTTGATCTTACCTTTGAACTTGAAGTGAAGAAATGATTTTGGAGTCC 960
Qy 963 AAACCTCTACATAAAGAAAGGCTCTGGCAAGGAGGAGGATATGAGGAAATGC 1022
Db 961 AAACCTCTACATAAAGAAAGGCTCTGGCAAGGAGGAGGATATGAGGAAATGC 1020
Qy 1023 GATTTCTCTCAGACATGTCTTCTTCAAGACGACCTTGACTCTGTCCAGAGGAGTTTCATA 1082
Db 1021 GATTTCTCTCAGACATGTCTTCTTCAAGACGACCTTGACTCTGTCCAGAGGAGTTTCATA 1080
Qy 1083 ATTTTCAACAGAGAAAGAGTAAACAGGAGCTTTAAACAAAGACACAAATCTAGCCTTG 1142
Db 1081 ATTTTCAACAGAGAAAGAGTAAACAGGAGCTTTAAACAAAGACACAAATCTAGCCTTG 1140
Qy 1143 GAACAAACCAAGACCCCAAGGTGAGGATGGTTCAGAAATAACA 1185
Db 1141 GAACAAACCAAGACCCCAAGGTGACAAATGGACAAATGGACA 1183

RESULT 9
AAS06704
ID AAS06704 standard; cDNA; 981 BP.
XX
AC AAS06704;
XX
DT 12-SEP-2001 (first entry)
XX
DE Polynucleotide sequence encoding human protein kinase #4.
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN W0200138503-A2.

XX 31-MAY-2001.
PD 22-NOV-2000; 2000WO-US032085.
XX 24-NOV-1999; 99US-0167482P.
PR (SUGS-) SUGEN INC.
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX WPI; 2001-343950/36.
DR P-PSDB; AAU03504.
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX Example 1; Fig 1; 433pp; English.
XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy, and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 981 BP; 294 A; 207 C; 245 G; 235 T; 0 U; 0 Other;

Query Match 56.0%; Score 831.2; DB 4; Length 981;
Best Local Similarity 90.7%; Pred. No. 5.2e-220;
Matches 903; Conservative 0; Mismatches 78; Indels 15; Gaps 1;
Qy 3 ATGGGAGCGAACACTTCAAGAAACCCAGCTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAACACTTCAAGAAACCCAGCTGTTGATGAAATGAAGATGTCAACTTT 60
Qy 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGCTTTGGGAGGTCTGCATTGTA 122
Db 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGCTTTGGGAGGTCTGCATTGTA 120
Qy 123 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAACAAAGTGGTG 182
Db 121 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAACAAAGTGGTG 180
Qy 183 GAGCGCAATGAAGTGAAGTGAAGTGTCTTCAAGGAACTCCAGATCATGCGGTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAAGTGAAGTGTCTTCAAGGAACTCCAGATCATGCGGTCTGGAGCAC 240
Qy 243 CCTTCTCTGTTAATTTGTTGTTATTCCTTCCAGATGAGGAAAGACATGTTTCATGTTGTTG 302
Db 241 CCTTCTCTGTTAATTTGTTGTTATTCCTTCCAGATGAGGAAAGACATGTTTCATGTTGTTG 300
Qy 303 GACCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAAGAACGTCCTCAAGGAA 362
Db 301 GACCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAAGAACGTCCTCAAGGAA 360
Qy 363 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAACCCAG 422
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGGCCCTGGACTACCTGCAGAACCCAG 420

QY 423 CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACGTG 482
Dd |||||
QY 421 CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACGTG 480
Dd |||||
QY 483 CACATCAGAGTTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 542
Dd |||||
QY 481 CACATCAGAGTTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540
QY 543 GCTGGCACCAGCCTTACATGGCACCCTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT 602
Dd |||||
QY 541 GCTGGCACCAGCCTTACATGGCACCCTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT 600
QY 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 662
Dd |||||
QY 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 660
QY 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACAGTTTGAGACG 722
Dd |||||
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACAGTTTGAGACG 720
QY 723 ACTGTTGTAACCTTACCCTTCTGCTGCTCACAGGAAATGCTGCTTCTTAAAAAGCTA 782
Dd |||||
QY 721 ACTGTTGTAACCTTACCCTTCTGCTGCTCACAGGAAATGCTGCTTCTTAAAAAGCTA 780
QY 783 CTCGACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 842
Dd |||||
QY 781 AGAAGGAAGACTGCATGTC-----CAAACGAAGTAACAAAAGGAAGCAGG 825
QY 843 ATGATGATATAAACTGGGATGCGATTTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 902
Dd |||||
QY 826 CTCTGCTGCTTAAGTTTAGAAGTTAGTATACATATTTGGGACACCAACTGTCTTCTTCTG 885
QY 903 AATAAGGAGGCTGAATTTGATCTTACCTTTGAACTTTGAGGAAATGATTTTGGAGTCC 962
Dd |||||
QY 886 CAGAAAGGAGGCTGAATTTGATCTTACCTTTGAACTTTGAGGAAATGATTTTGGAGTCC 945
QY 963 AAACCTCTACATAAAGAAAAAAGCCTCTGGCAAAG 998
Dd |||||
QY 946 AAACCTCTACATAAAGAAAAAAGCCTCTGGCAAAG 981

RESULT 10
ABA08463
ID ABA08463 standard; cDNA; 678 BP.

XX ABA08463;
AC ABA08463;
XX
XX
DT 11-JAN-2002 (first entry)
XX
DE Human Ser/Thr kinase homologue-encoding cDNA, SEQ ID NO:239.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
XX 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX

PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR P-PSDB; ABB11219.
DR
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
PS
XX
XX Claim 1; Page 422; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 678 BP; 203 A; 148 C; 152 G; 175 T; 0 U; 0 Other;

Query Match 45.3%; Score 672.8; DB 4; Length 678;
Best Local Similarity 99.7%; Pred. No. 4.1e-176;
Matches 674; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 441 ATGAAGCCTGACAAATATTTTACTTGACGAACATGGGACATGCACATCAGATTTCAC 500
Dd |||||
Dd 1 ATGAAGCCTGACAAATATTTTACTTGACGAACATGGGACATGCACATCAGATTTCAC 60
QY 501 ATTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATGGCTGGCACCAGCCTTAC 560
Dd |||||
Dd 61 ATTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATGGCTGGCACCAGCCTTAC 120
QY 561 ATGGCACCTGAGATGTTTCAAGTCCAGAAAGGAGCAGGCTATTCCTTGTGACTGG 620
Dd |||||
Dd 121 ATGGCACCTGAGATGTTTCAAGTCCAGAAAGGAGCAGGCTATTCCTTGTGACTGG 180
QY 621 TGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCCGAGACCGTATCATATTTCG 680

Db 181 TGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGCGGAGACCGTATCATATTCGC 240
Qy 681 TCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAGACGACTGTTGTAACCTTACCCT 740
Db 241 TCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAGACGACTGTTGTAACCTTACCCT 300
Qy 741 TCTGCCTGGTCCAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTTAATCCAGAC 800
Db 301 TCTGCCTGGTCCAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTTAATCCAGAC 360
Qy 801 CAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAACTGG 860
Db 361 CAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAACTGG 420
Qy 861 GATGAGTTTTCAGAGAGGCTCATTCAGGTTTTCATTCCTTAATAAGGCGGCTGAAT 920
Db 421 GATGAGTTTTCAGAGAGGCTCATTCAGGTTTTCATTCCTTAATAAGGCGGCTGAAT 480
Qy 921 TGTGATCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAA 980
Db 481 TGTGATCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAA 540
Qy 981 AAAAGCTCTGGCAAAGAGGAGGATATGAGGAAATGCGATTTCTTCTCAGACATGT 1040
Db 541 AAAAGCTCTGGCAAAGAGGAGGATATGAGGAAATGCGATTTCTTCTCAGACATGT 600
Qy 1041 CTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCATAATTTTCAACAGAGAAAAA 1100
Db 601 CTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCATAATTTTCAACAGAGAAAAA 660
Qy 1101 GTAAACAGGGACTTTA 1116
Db 661 GTAAACAGGGACTGTA 676

RESULT 11

AAD23677
ID AAD23677 standard; cDNA; 711 BP.
AC AAD23677;
XX
DT 07-MAR-2002 (first entry)
XX Novel human protein (NHP) kinase cDNA #2.
DE Novel human protein (NHP) kinase cDNA #2.
XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutritional; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic;
KW SS.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..711
FT /*tag= a
FT /product= "Novel human protein (NHP) kinase"
XX
PN WO200181557-A2.
XX
PD 01-NOV-2001.
XX
PF 24-APR-2001; 2001WO-US013149.
XX
PR 25-APR-2000; 2000US-0199499P.
PR 01-MAY-2000; 2000US-0201227P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
XX WPI; 2002-034442/04.
DR P-PSDB; AAE14259.

XX New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.
XX
PS Disclosure; Page 40; 44pp; English.
XX
CC The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase cDNA which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-
CC dependent kinases cDNA related to the invention
XX
SQ Sequence 711 BP; 199 A; 153 C; 181 G; 178 T; 0 U; 0 Other;

Query Match 44.2%; Score 656.2; DB 6; Length 711;
Best Local Similarity 99.5%; Pred. No. 1.7e-171;
Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGGAGCGAACACTTCAAGAAAAACCCAGGTGTTGATGAAAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAACACTTCAAGAAAAACCCAGGTGTTGATGAAAAATGAAGATGTCAACTTT 60
Qy 63 GACCACCTTTGAAATTTTGGAGGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCATTGTA 122
Db 61 GACCACCTTTGAAATTTTGGAGGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCATTGTA 120
Qy 123 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAAAGTGCCTG 182
Db 121 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAAAGTGCCTG 180
Qy 183 GAGCGCAATGAAGTGAAGTGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC 242
Db 181 GAGCGCAATGAAGTGAAGTGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC 240
Qy 243 CTTTCTCTGTTAATTTGGTATTCTCTTCCAAAGATGAGGAAGACATGTTTCATGTTGTTG 302
Db 241 CTTTCTCTGTTAATTTGGTATTCTCTTCCAAAGATGAGGAAGACATGTTTCATGTTGTTG 300
Qy 303 GACCTCTCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCTCAAGGAA 362
Db 301 GACCTCTCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCTCAAGGAA 360
Qy 363 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGCGCTGGACTACCTGCAGAACCCAG 422
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGCGCTGGACTACCTGCAGAACCCAG 420
Qy 423 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG 480
Qy 483 CACATCACAGATTTCAACATTTGTCGATGCTGCCAGGAGACACAGATTACCACCATG 542
Db 481 CACATCACAGATTTCAACATTTGTCGATGCTGCCAGGAGACACAGATTACCACCATG 540
Qy 543 GCTGGCACCAGCCTTACATGGCAGCTGAGATGTTTCCAGCTCCAGAAAAGGAGCAGCTAT 602
Db 541 GCTGGCACCAGCCTTACATGGCAGCTGAGATGTTTCCAGCTCCAGAAAAGGAGCAGCTAT 600
Qy 603 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATGCTGAGAGGCCGG 662

Db 601 TCCCTTGTCTGACTGGTGGTCCCTGGGAGTGACGGCATATGAAGTCTGTGAGAGGCCGG 660
QY 663 A 663
Db 661 A 661

RESULT 12
AAD23676
ID AAD23676 standard; cDNA; 678 BP.

XX AAD23676;
AC
XX 07-MAR-2002 (first entry)
DT Novel human protein (NHP) kinase cDNA #1.

DE Novel human protein; NHP; gene therapy; diagnosis; drug screening;
XX gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic;
KW ss.

XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1..678
FT /*tag= a
FT /product= "Novel human protein (NHP) kinase"

PN WO200181557-A2.
XX
XX 01-NOV-2001.
PD
XX 24-APR-2001; 2001WO-US013149.
PF

XX 25-APR-2000; 2000US-0199499P.
PR 01-MAY-2000; 2000US-0201227P.
XX
XX (LEXI-) LEXICON GENETICS INC.

PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
XX
DR WPI; 2002-034442/04.
DR P-PSDB; AAE14258.

XX New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.

XX Disclosure; Page 39; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase cDNA which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-
CC dependent kinases cDNA related to the invention

XX
SQ Sequence 678 BP; 195 A; 148 C; 179 G; 156 T; 0 U; 0 Other;
Query Match 44.1%; Score 655.2; DB 6; Length 678;
Best Local Similarity 99.5%; Pred. No. 3.2e-171;

Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 ATGGGAGCGAAACACTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAAACACTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60
QY 63 GACCACCTTTGAAATTTGGAGCCATTGGGAAAGGACGTTTGGGAGGTCTGCAATTGTA 122
Db 61 GACCACCTTTGAAATTTGGAGCCATTGGGAAAGGACGTTTGGGAAAGGTCTGCAATTGTA 120
QY 123 CAGAAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCCTG 182
Db 121 CAGAAGAATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCCTG 180
QY 183 GACGCAATGAAGTGAAGTGTCTTCAAGGAACCTCCAGATCATGCAGGTCTGGAGCAC 242
Db 181 GACGCAATGAAGTGAAGTGTCTTCAAGGAACCTCCAGATCATGCAGGTCTGGAGCAC 240
QY 243 CCTTTCCTGGTTAATTTGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGTTGGTG 302
Db 241 CCTTTCCTGGTTAATTTGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGTTGGTG 300
QY 303 GACCTCCTGCTGGTGGAGACCTGCGTTATACCTGAAACAGAACGTCCACTTCAAGGAA 362
Db 301 GACCTCCTGCTGGTGGAGACCTGCGTTATACCTGAAACAGAACGTCCACTTCAAGGAA 360
QY 363 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGATGCGCTGGACTACCTGCAGAAC 422
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGATGCGCTGGACTACCTGCAGAAC 420
QY 423 CGCATCATTCACAGGGATATGAAGCCTGACCAATATTTTACTTGACGAACATGGGCACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCCTGACCAATATTTTACTTGACGAACATGGGCACGTG 480
QY 483 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542
Db 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 540
QY 543 GCTGGCACCAAGCCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 602
Db 541 GCTGGCACCAAGCCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
QY 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAAGTGTGAGAGGCCGG 662
Db 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAAGTGTGAGAGGCCGG 660

RESULT 13
ABQ61051

ID ABQ61051 standard; cDNA; 1587 BP.

XX AC ABQ61051;

XX 26-FEB-2003 (first entry)

DE Serine/threonine kinase encoding sequence.

XX Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14;
KW cytostatic; anti-inflammatory; gene therapy; nutritional supplement;
KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnery; gene; ss.

XX Homo sapiens.

XX WO200231111-A2.

PD 18-APR-2002.

PF 11-OCT-2001; 2001WO-US027760.

PR 12-OCT-2000; 2000US-00687527.

XX

PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-426278/45.
DR N-PSDB; ABP43807.
XX
PT New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.
XX
PS Claim 1; SEQ ID # 264; 357pp + Sequence Listing; English.
XX
CC The invention relates to 446 newly isolated polynucleotide sequences. The
CC activity of polynucleotides of the invention may be described as,
CC vulnery, neuroprotective, immunomodulator, cytostatic and anti-
CC inflammatory. Compositions comprising nucleic acids of the invention are
CC useful for treating a mammalian subject, or as nutritional sources or
CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABQ60788-
CC ABQ61233 represent polynucleotides of the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1587 BP; 414 A; 421 C; 425 G; 327 T; 0 U; 0 Other;
Query Match 36.4%; Score 540.8; DB 6; Length 1587;
Best Local Similarity 69.1%; Pred. No. 2.8e-139;
Matches 772; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
QY 3 ATGGGAGCGAACACTTCAAGAAACACCCAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGGCGGAACCACTCCACAAAGCCCCCGTGTGACGAGAATGAGGAAGTCAACTTT 60
QY 63 GACCACCTTGAATTTTGGAGGCCATTGGGAAAGGCGAGTTTGGGGAGGTCTGCAATTGTA 122
Db 61 GACCATTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCAATCTG 120
QY 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGATGAAATGAAGTGAAGTGCATC 182
Db 121 CAGAAGCGAGACACTAAGAAATGTATGCAATGAAGTACATGAAAGCAGAAAGTGCATC 180
QY 183 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGTCTGGAGCAC 242
Db 181 GAGAGGATGAGGTTCGGAATGTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGAGCAC 240
QY 243 CCTTCTCTGTTAATTTGTGTTATCTTCCAAAGATGAGGAGACATGTTTATGTTGGTG 302
Db 241 CCTTCTCTGTTCAATCTGTGTTACTCTTCCAGGATGAGGAGACATGTTTATGTTGGTG 300
QY 303 GACCTCTCTGTTGGTGAGACCTGCGTTATCACCTGCAACAGAACGTCCTCAAGGAA 362
Db 301 GACCTGCTCTGGAGGCGACCTGCGCTACCATCTGCAGCAGATGTGCAATTCACAGAG 360
QY 363 GAAACAGTGAAGCTCTTCACTGTGAGTGGTTCATGCGCCCTGGACTACCTGCAGAACCCAG 422
Db 361 GGGACTGTGAACCTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTAC 420
QY 423 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACCAACATGGGCACGTG 482
Db 421 CACATCATTCACAGAGACATCAAGCCAGACAATATCTCTGTGATGAACACGGACATGTT 480
QY 483 CACATCACAGATTTCAACATGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542
Db 481 CACATTCACAGACTTCAACATAGCGAGCGGTAGTGAAGGAGCAGAAAGGGCTTCTCCATG 540
QY 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCTCTCCAGAAAGGAGCA 596

Db 541 GCTGGCACCAAGCCTTACATGGCTCCAGAAATATTCAGGTGTACATGACAGAGCCCC 600
QY 597 GGCTATTCCTTTGCTGTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGA 656
Db 601 GGATACTCGTACCTGTGCTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCGG 660
QY 657 GGCCGGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATGTACACACGTTT 716
Db 661 GGCTGGAGGCGGTACGAAATCCACTCGGTCCAGCCCATCGATGAATCTCTCAACATGTTT 720
QY 717 GAGACGACTGTGTTAACTTACCTTCTGCTGGTGCACAGGAAATGCTGCTCACTTCTTAAA 776
Db 721 AAGTGGAGCGTGTCCACTACTCTCTCCAGTGGTCAAGGGGATGCTGCTGAGG 780
QY 777 AAGTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC 836
Db 781 AAGTCTCTGACCAAGGATCTGTAGAGCGCGGTGTCCAGCCTTCATGACATACAGAGCGTG 840
QY 837 CCGTATATGATGATATAAATCTGGGATGAGTGTTCAGAAAGAGGCTCATTCAGGTTTC 896
Db 841 CCTACTTGGCGACATGAATGGAACGCGGTGTTCAAGAAAGGCACTGATGCCCGCTTT 900
QY 897 ATTCTTAATAAGGCGAGCTGAATGTGATCTCTTCAAGAGCACCTTGTCTGCTCCAGAAAG 956
Db 901 GTGCCCCAATAAAGGAGGTGTAATGCGATGCCATTCACATTTGAGCTTGAAGAGATGATTCTA 960
QY 957 GAGTCCAAACCTCTACATAAGAAAGGCTCTGGCAAGAA---GGAGAAAGGATATG 1013
Db 961 GAATCCAAAGCCACTTCAAAAAGAGAGAGGATGGCAAGAACAGATCCAGGGATGGC 1020
QY 1014 AGGAAATGCGATTTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGTCTGCTCCAGAAAG 1073
Db 1021 ACAAGGACAGCTGCCCGCTGAATGGACACCTGACACTGTTTGGAGACTGCTCCGGGAG 1080
QY 1074 GAGTTCATAATTTTCAACAGAGAAAGTAAACAGGGA 1111
Db 1081 GAATTCATCATATTTCAACAGAGAGAGAGCTCAGGAGGCA 1118

RESULT 14

AAF44625

ID AAF44625 standard; cDNA; 3224 BP.

XX AAF44625;

XX AC AAF44625;

XX XX 27-MAR-2001 (first entry)

XX DT 27-MAR-2001 (first entry)

XX DE Novel protein kinase cDNA, SEQ ID NO: 4.

XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

XX KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;

XX KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;

XX KW immune disorder; cardiovascular disease; neurodegenerative disease;

XX KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

XX KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX OS Homo sapiens.

XX XX WO200073469-A2.

XX FN 07-DEC-2000.

XX PD 26-MAY-2000; 2000WO-US014842.

XX XX 28-MAY-1999; 99US-0136503P.

XX XX (SUGEN-) SUGEN INC.

XX PA Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX PI WPI; 2001-032161/04.

XX DR P-PSDB; AAB65600.

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX
PS Example 1; Fig 2; 310pp; English.
XX
CC The present sequence encodes a novel protein kinase. The nucleic acids
CC and the protein kinases they encode may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 3224 BP; 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other;
Query Match 36.4%; Score 540.8; DB 4; Length 3224;
Best Local Similarity 69.1%; Pred. No. 4e-139;
Matches 772; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
QY 3 ATGGGAGCGAACACTTCAAGAAACCAACCAGTGTGATGAATGAAGATGTCAACTTT 62
DB 65 ATGGGCGGAACCACTCCCAAGCCCCCGTGTGACGAGATGAGGAAGTCAACTTT 124
QY 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCATTGA 122
DB 125 GACCAATTTTCAGATTCTGGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCATCGT 184
QY 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATGAATGAAGTCCGTG 182
DB 185 CAGAAGCGAGACACTAAGAAATGTATGCAATGAATGAATGAAGTCAAGTGCATC 244
QY 183 GAGCGCAATGAAGTGAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGGAGCAC 242
DB 245 GAGAGGATGAGGTTCGGAATGTTTCCGGAGCTGCAGATCATGCAAGGGCTGGAGCAC 304
QY 243 CCTTCTCGTTAATTGTTGTTATCTTCCCAAGATGAGGAAGACATGTTTCATGTTGGT 302
DB 305 CCTTCTCGTTAATTGTTGTTATCTTCCAGGATGAGGAGGACATGTTTCATGTTGGT 364
QY 303 GACCTCTGCTGGGTGGAGACCTGCTTATCACCTGCAACAGAGAGCTCCACTTCAAGGAA 362
DB 365 GACCTGCTCTGGGAGGCGACCTGCGTACCATCTGCAGCAGATGTGCATTTCAAGAG 424
QY 363 GAAACAGTGAAGCTTTCATCTGTGAGTGGTTCATGGCCCTGGACTACCTGCAGAACCCAG 422
DB 425 GGGACTGTGAAGCTTACATCTGTGAGTGGCACTGGCCCTGGAGTATCTTCAGAGGTAC 484
QY 423 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGAAGAACATGGGCACGTG 482
DB 485 CACATCATCCACAGAGACATCAAGCCAGACAATATCTCTGCTGGATGAACACGGACATGTT 544
QY 483 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542
DB 545 CACATTACAGACTTCAACATAGCGACGGTAGTGAAGGAGCAGAAAGGGCTTCTCCCATG 604
QY 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTT-----AGTCCAGAAAGGAGCA 596
DB 605 GCTGGCACCAAGCCTTACATGGCTCCAGAAAGTATTCAGGTGTATATGACAGAGGCCCC 664
QY 597 GGCTATTCTTTGCTGTTGACTGGTGTCTCGGGAGTGACGGCATATGAATGCTGTAGA 656

DB 665 GGATACTCGTACCCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGTGCGG 724
QY 657 GCGCGGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATGTACACACGTTT 716
DB 725 GGCTGGAGGCCGTACGAATCCCACTGGTCCAGCCCATCGATGAATCCTCAACATGTT 784
QY 717 GAGACGACTGTTGTAACCTTACCCCTTCTGCTGGTTCAGAGAAATGGTGTCACTTCTTAA 776
DB 785 AAGGTGGAGCGTGTCCACTACTCTCCAGCTGGTGCAGGGGATGGTCCCTGTGAGG 844
QY 777 AAGCTACTCGAACCTTATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACCTTC 836
DB 845 AAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCCTTCATGACATACAGAGCGTG 904
QY 837 CCGTATATGAATGATATAAACTGGGATGCAGTTCCTTTCAGAAAGGCTCATTCAGGTTTC 896
DB 905 CCTACTTGGCCGACATGAATGGGACGCGGTGTTCAAGAAAGGCACTGATGCCCGGCTTT 964
QY 897 ATTCTTAATAAAGGCGAGGCTGAATGTGATCCTTCTTCAAGAGACCTTGACTCTGTCCAGAAG 956
DB 965 GTGCCCAATAAAGGGAGGTGAATCGCATCCCACTTTCAGCTTGAAGAGATGATTTCTA 1024
QY 957 GAGTCCAAACCTCTACATAAAGAAAAAAGCGTCTGCGCAAGAA---GGAGAAAGGATATG 1013
DB 1025 GAATCCAAAGCCACTTCAAAAAAAGAAAGCGATTGGCAAAAGAACAGATCCAGGGATGGC 1084
QY 1014 AGGAAATGCGATTCTTCTCAGACATGTCTTCTTCAAGAGACCTTGACTCTGTCCAGAAG 1073
DB 1085 ACAAGGACAGCTGCCCGTGAATGGACACCTGCAGCACTGTTGGAGACTGTCCCGGAG 1144
QY 1074 GAGTTCATAATTTTCAACAGAGAAAGTAAACAGGGA 1111
DB 1145 GAATTCATCATATTCAACAGAGAGAGCTCAGGAGGCA 1182
RESULT 15
ADA19317
ID ADA19317 standard; cDNA; 3224 BP.
XX
AC ADA19317;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human insulin resistance marker IRM210 (Ser/Thr protein kinase) cDNA #2.
XX
KW Insulin resistance; IR; susceptibility; diagnosis;
KW insulin resistance marker; IRM; polymorphism; genotype; hypertension;
KW dyslipidaemia; type 2 diabetes; obesity; coronary artery disease;
KW drug screening; antidiabetic; cardiant; antilipaeamic; hypotensive; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200298355-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017227.
XX
PR 01-JUN-2001; 2001US-0295264P.
XX
PA (CLIN-) CLINGENIX INC.
XX
PI Ma Y, Lih C, Chen F, Fairman J, Chen YI;
XX
DR WPI; 2003-148601/14.
XX
PT Diagnosing for insulin resistance (IR) an IR-related condition, e.g.
PT hypertension, diabetes or obesity, comprises detecting an altered or a
PT difference in expression of insulin resistance marker (IRM) genes in a
PT sample from the subject.
XX
PS Claim 1; Page; 125pp; English.

XX The invention relates to a method for diagnosing insulin resistance (IR),
CC an IR-related condition, or susceptibility to IR or an IR-related
CC condition in a patient. The method comprises detecting a difference in
CC expression of at least one insulin resistance marker (IRM) in a
CC biological sample from the patient, compared to the level of expression
CC of the IRM in reference individuals who are not insulin resistant. The
CC invention also encompasses screening for an agent to determine its
CC usefulness in treating IR; the identification of a polymorphism
CC associated with an IR phenotype or risk of developing IR; estimating the
CC frequency of a haplotype for a set of nucleotide polymorphism markers in
CC a population; detecting an association between a haplotype and a
CC phenotype; and identifying genes associated with a disease state. The
CC methods of the invention are useful for diagnosing insulin resistance
CC (IR), an IR-related condition, or susceptibility to IR or an IR-related
CC condition. Such conditions include hypertension, dyslipidaemia, type 2
CC diabetes, obesity or coronary artery disease. The methods are also useful
CC in screening for agents useful in the treatment of these disorders. The
CC present sequence represents an IRM cDNA which is specifically claimed for
CC use in the method of the invention. Note: The present sequence is not
CC shown in the specification, but was obtained from GenBank using the
CC accession number listed in Table 1 (page 25-33).

XX
SQ Sequence 3224 BP; 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other;
Query Match 36.4%; Score 540.8; DB 7; Length 3224;
Best Local Similarity 69.1%; Pred. No. 4e-139;
Matches 772; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

Qy	3	ATGGGAGCGAACACTTCAAGAAACCCACCACTGTTTGATGAAATGAAGATGTCAACTTT	62
Db	65	ATGGGCGGAACCACTCCACAAAGCCCCCGTGTGACGAGAATGAGGAAGTCAACTTT	124
Qy	63	GACCACATTTGAAATTTTGGAGGCCATTTGGAAAGGCGAGTTTGGGAGGCTGCTGCAATTGA	122
Db	125	GACCATTTTCAGATTCTGCGGGCCATTTGGTAAGGGAGTTTGGAAAGGTATGCATCGTG	184
Qy	123	CAGAAGATGATACCAAGAGATGTGGCAATGAAGTACATGATGATGATGATGATGATGATG	182
Db	185	CAGAAGCGGAGACACTAAGAAATGATGCAATGAAGTACATGATGATGATGATGATGATG	244
Qy	183	GAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGCTGCGAGCAC	242
Db	245	GAGAGGATGAGGTTTCGGAATGTTTCCGGGAGCTGCAGATCATGCAAGGCTGCGAGCAC	304
Qy	243	CCTTCTCTGGTTAATTTGTGGTATTCCTTCAAGATGAGGAGACATGTTTCAATGGTGGTG	302
Db	305	CCCTTCTCTGGTCAATCTGTGGTACTCTCTCCAGGATGAGGAGACATGTTTCAATGGTGGTG	364
Qy	303	GACCTCTCTGGTGGGAGACCTGCGTATCACCTGCAACAGAACGCTCCACTTCAAGGAA	362
Db	365	GACCTGCTCTGGGAGCGGACCTGCGTACCATCTGCAGCAGAAATGTGCATTTTCACAGAG	424
Qy	363	GAAACAGTGAAGCTCTTCAATCTGTGAGCTGGTCAATGAGGAGGAGGAGGAGGAGGAG	422
Db	425	GGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTAC	484
Qy	423	CGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGACCTG	482
Db	485	CACATCATTCACAGAGACATCAAGCCAGACAAATATCTCTGTGGATGAACACGGACATGTT	544
Qy	483	CACATCACAGATTTCAACATTTGCTGGATGCTGCCCCAGGGAGACACAGATTACCAACATG	542
Db	545	CACATTACAGACTTCAACATAGCGGACGGTAGTGAAGGAGCAGAAAGGGCTTCTCTCATG	604
Qy	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTT-----AGCTCCAGAAAGGAGCA	596
Db	605	GCTGGCACCAAGCCTTACATGGCTCCAGAAATGATTTCCAGGTGATGACAGAGGCCCC	664
Qy	597	GGCTATTCTTTGCTGTGTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGA	656
Db	665	GGATACTCGTACCCTGTTCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCGG	724

Qy	657	GGCCGGAGACCGGTATCATATTTCCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTT	716
Db	725	GGCTGGAGGCGGTACGAAATCCACTCGGTCAAGCCCATCGATGAATCTTCAACATGTTT	784
Qy	717	GAGACGACTGTTGTAACCTTACCTTCTGCTGCTGTCACAGGAAATGGTGTCTTATAA	776
Db	785	AAGTGGAGCGGTGTCCACTACTCTCCACGTGTGTCAGGGGATGGTGGCCCTGCTGAGG	844
Qy	777	AAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC	836
Db	845	AAGCTCTGACCAAGGATCTTGAGAGCCGCGTGTCCAGCCTTTCATGACATACAGAGCGTG	904
Qy	837	CCGTATATGAATGATATAAAGCTGGGATGAGTTTTCAGAAAGAGGCTCATTCAGGTTTC	896
Db	905	CCCTACTTGGCCGACATGAACCTGGGACGCGGTGTTCAGAAAGGCACTGATGCCCGCTTT	964
Qy	897	ATTCTTAATAAAGGAGGCTGAATTTGATCCTTACCTTTGAACTTGAGGAAATGATTTTG	956
Db	965	GTGCCCATAAAGGAGGTTGAACCTGCGATCCCACTTTCAGCTTGAAGAGATGATTTCTA	1024
Qy	957	GAGTCCAAACCTCTACATAAGAAAGGCGTCTGCGCAAGAA--GGAGAGGATATG	1013
Db	1025	GAATCCAAAGCCACTTCACAAAAGAGAGCGGATTTGGCAAGAACAGATCCAGGATGGC	1084
Qy	1014	AGGAAATGCGATTCTTCTCAGACATGCTCTTCTTCAAGAGCACCTTGACTCTGTCAGAG	1073
Db	1085	ACAAAGGACAGCTGCGCGCTGAATGGACACCTTGACACACTGTTTGGAGACTGTCGGGAG	1144
Qy	1074	GAGTTCATTAATTTTCAACAGAGAAAGTAAACAGGGA	1111
Db	1145	GAATTCATCATATTTCACACAGAGAGAGCTCAGGAGGCA	1182

Search completed: June 26, 2004, 21:12:27
Job time : 473 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:03:31 ; Search time 4048 Seconds
(without alignments)
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Title: US-10-667-442-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	1485	100.0	1485	6	AR432044	Sequence AR432044
3	1228.6	82.7	1281	6	AX320934	Sequence AX320934
4	1188.2	80.0	1594	6	AX207388	Sequence AX207388
5	1188.2	80.0	1594	6	AX766348	Sequence AX766348
6	1186.2	79.9	1191	6	AR393903	Sequence AR393903
7	1186.2	79.9	1191	6	AX303185	Sequence AX303185
8	1184.6	79.8	1191	6	AX320936	Sequence AX320936
9	1162.6	78.3	1675	6	AR393904	Sequence AR393904
10	1162.6	78.3	1675	6	AX303187	Sequence AX303187
11	1160.6	78.2	1224	6	AR393902	Sequence AR393902
12	1160.6	78.2	1224	6	AX303183	Sequence AX303183
13	1029.4	69.3	2063	6	AX833107	Sequence AX833107
14	1029.4	69.3	2063	9	AK094580	Sequence AK094580
15	831.2	56.0	981	6	AX166513	Sequence AX166513
16	792.4	53.4	4973	10	BC055002	Sequence BC055002
17	656.2	44.2	711	6	AR393901	Sequence AR393901
18	656.2	44.2	711	6	AX303181	Sequence AX303181
19	655.2	44.1	678	6	AR393900	Sequence AR393900
20	655.2	44.1	678	6	AX303179	Sequence AX303179
21	556.8	37.5	3367	10	BC058412	Sequence BC058412
22	556.8	37.5	3367	10	BC052404	Sequence BC052404
23	556.8	37.5	3449	10	BC056396	Sequence BC056396
24	553.6	37.3	2045	10	MMU250840	Sequence AJ250840
25	540.8	36.4	3224	6	AX056360	Sequence AX056360
26	540.8	36.4	3224	9	HSA250839	Sequence AJ250839
27	539.2	36.3	3236	9	BC038238	Sequence BC038238
28	516.4	34.8	3244	6	AX376504	Sequence AX376504
29	516.4	34.8	3244	9	AY358353	Sequence AX376504
30	494.4	33.3	2184	10	BC026457	Sequence AY358353
31	494.4	33.3	2201	10	AB041542	Sequence BC026457
32	481.6	32.4	1257	6	AR411704	Sequence AB041542
33	481.6	32.4	1826	6	AR411703	Sequence AR411704
34	481.6	32.4	2143	9	AY098866	Sequence AR411703
35	480	32.3	1487	6	AX504245	Sequence AY098866
36	480	32.3	1858	9	BC015792	Sequence AX504245
37	476.2	32.1	1787	6	AX056359	Sequence BC015792
38	469.6	31.6	827	9	BC021666	Sequence AX056359
39	468.4	31.5	2028	9	BC045760	Sequence BC021666
40	466.8	31.4	1864	6	AX642304	Sequence BC045760
41	462	31.1	1591	6	AX768900	Sequence AX642304
42	458.2	30.9	1640	6	AX179651	Sequence AX768900
43	457.4	30.8	2038	9	AB056389	Sequence AX179651
44	445.4	30.0	1868	9	AK057849	Sequence AB056389
45	441.8	29.8	2182	6	AX364903	Sequence AK057849

ALIGNMENTS

RESULT 1
AR265353
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR265353
Sequence 1 from patent US 6492155.
AR265353
AR265353.1 GI:29693863
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1485)
Ye, J., Yan, C., Di Francesco, V. and Beasley, E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
Patent: US 6492155-A 1 10-DEC-2002;

linear PAT 10-APR-2003

FEATURES		Location/Qualifiers	
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Best Local Similarity		100.0%;	Pred. No. 0;
Matches 1485;		Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
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Db	1	CCATGGAGCGGAACAC	TTCAAGAAACCCACCAAGTGTGATGAAATGAAGATGTCAACT 60
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Db	181	TGGAGCGCAATGAAG	TGAGAAATGCTTCAAGGAACCTCCAGATCATGCGGGTCTGGAGC 240
Qy	241	ACCTTTCTCTGTTAA	TTTGTGGTATCTCTTCCAGATGAGGAAGACATGTTTCATGTTGG 300
Db	241	ACCTTTCTCTGTTAA	TTTGTGGTATCTCTTCCAGATGAGGAAGACATGTTTCATGTTGG 300
Qy	301	TGGACCTCTGCTGGT	GGAGACCTGCGTTATCACCTGCAACAGAACCTTCAAGG 360
Db	301	TGGACCTCTGCTGGT	GGAGACCTGCGTTATCACCTGCAACAGAACCTTCAAGG 360
Qy	361	AAGAAACAGTGAAGC	TCTTCACTGTGAGCTGGTCAATGAGCTGAGTACCTGCAGAAC 420
Db	361	AAGAAACAGTGAAGC	TCTTCACTGTGAGCTGGTCAATGAGCTGAGTACCTGCAGAAC 420
Qy	421	AGCGCATCAATTCAC	AGGGATATGAAGCTGACAAATATTTTACTTGACGAACATGGGCACG 480
Db	421	AGCGCATCAATTCAC	AGGGATATGAAGCTGACAAATATTTTACTTGACGAACATGGGCACG 480
Qy	481	TGCACATCAGAGATT	TTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTACCACCA 540
Db	481	TGCACATCAGAGATT	TTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTACCACCA 540
Qy	541	TGGCTGGCACCAAGC	CTTACATGGCACCTGAGATGTTTCCAGCTCCAGAAAGGAGCAGGCT 600
Db	541	TGGCTGGCACCAAGC	CTTACATGGCACCTGAGATGTTTCCAGCTCCAGAAAGGAGCAGGCT 600
Qy	601	ATTCTTTTGTGTTG	ACTGTTGCTGGAGTGACGGCATATGAAGTCTGAGAGGCC 660
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Qy	721	CGACTGTTGTAAC	TACTTACCTTCTGCTGGTACAGGAATGGTGTCACTTTTAAAAAGC 780
Db	721	CGACTGTTGTAAC	TACTTACCTTCTGCTGGTACAGGAATGGTGTCACTTTTAAAAAGC 780
Qy	781	TACTCGAACCTAAT	CCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Db	781	TACTCGAACCTAAT	CCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Qy	841	ATATGAATGATATA	AACTGGGATGCGATTTTTCAGAAAGGCTCATTTCCAGGTTTCATT 900
Db	841	ATATGAATGATATA	AACTGGGATGCGATTTTTCAGAAAGGCTCATTTCCAGGTTTCATT 900
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Qy	1021	GCGATTCTTCTCAG	ACATGTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTCA 1080
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RESULT 2

AR432044

LOCUS

AR432044

DEFINITION

Sequence 1 from patent US 6653117.

ACCESSION

AR432044

VERSION

AR432044.1 GI:40194241

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1485)

AUTHORS

Ye, J., Yan, C., Di Francesco, V. and Beasley, E.M.

TITLE

Isolated human kinase proteins

JOURNAL

Patent: US 6653117-A 1 25-NOV-2003;

FEATURES

Location/Qualifiers

1..1485

Source

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match

100.0%;

Score 1485;

DB 6;

Length 1485;

Best Local Similarity

100.0%;

Pred. No. 0;

Matches 1485;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

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Qy	61	TTGACCACTTTGAAAT	TTTGGAGCCATTTGGAAAGGCGAGTTTGGGGAGGTCTGCAATTG 120
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Qy	241	ACCTTTCTCTGTTAA	TTTGTGGTATCTCTTCCAGATGAGGAAGACATGTTTCATGTTGG 300
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Qy	541	TGGCTGGCACCAAGC	CTTACATGGCACCTGAGATGTTTCCAGCTCCAGAAAGGAGCAGGCT 600
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Qy	601	ATTCTTTTGTGTTG	ACTGTTGCTGGAGTGACGGCATATGAAGTCTGAGAGGCC 660
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Qy	661	GGAGACCGTATCAT	ATTCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGA 720
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Db	781	TACTCGAACCTAAT	CCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
Qy	841	ATATGAATGATATA	AACTGGGATGCGATTTTTCAGAAAGGCTCATTTCCAGGTTTCATT 900
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Qy	901	CTAATAAAGCGAG	CTGAATTTGTGATCTTACCTTTGAAGTGGGAATGATTTTGGAGT 960
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RESULT 5
AX766348
LOCUS AX766348 1594 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 44 from Patent WO0218557.
ACCESSION AX766348
VERSION AX766348.1 GI:32260298

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Gururajan,R., Hafalia,A.J., Patterson,C., Tribouley,C.M.,
Azimzai,Y., Ding,L., Yao,M.G., Yue,H., Au-Young,J., Bandman,O.,
Baughn,M.R., Burford,N., Burrill,J.D., Elliott,V.S., Gandhi,A.R.,
Ison,C.H., Kearney,L., Lal,P.G., Lu,D.A., Lu,Y., Tang,Y.T.,
Zingler,K.A., Marcus,G.A., Nguyen,D.B., Policky,J.L., Ramkumar,J.,
Thangavelu,K., Thornton,M., Walia,N.K. and Warren,B.A.
HUMAN KINASES

TITLE Patent: WO 0218557-A 44 07-MAR-2002;
JOURNAL Incyte Genomics Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="ID No: 7946584CB1"

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Query Match 80.0%; Score 1188.2; DB 6; Length 1594;
Best Local Similarity 99.7%; Pred. No. 2.7e-286;
Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGGGAGCGAACACTTCAAGAAACCAACAGTGTGTTGATGAAAATGAAGATGTCAACT 60
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QY 61 TTGACCACTTGAATTTTTCGAGCCATTTGGGAAAGGAGTGTGGGAGGTCTGCATTG 120
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QY 121 TACAGAAAGATGATACCAAGAAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
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RESULT 6
AR393903
LOCUS
DEFINITION Sequence 10 from patent US 6617147.
ACCESSION AR393903
VERSION AR393903.1 GI:40121079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1191)
AUTHORS Hu,Y., Nepomnichy,B., Wang,X. and Donoho,G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 10 09-SEP-2003;
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Query Match 79.9%; Score 1186.2; DB 6; Length 1191;
Best Local Similarity 99.7%; Pred. No. 8.4e-286;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGGGAGCGAACACTTCAAGAAACCACCAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
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RESULT 7
AX303185
LOCUS
DEFINITION Sequence 10 from Patent WO0181557.
ACCESSION AX303185
VERSION AX303185.1 GI:17383668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Hu,Y., Nepomnichy,B., Wang,X., Donoho,G., Scoville,J. and
Walke,D.W.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0181557-A 10 01-NOV-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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ORIGIN
Query Match 79.9%; Score 1186.2; DB 6; Length 1191;
Best Local Similarity 99.7%; Pred. No. 8.4e-286;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGGGAGCGAACACTTCAAGAAACCACCAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
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QY 63 GACCACCTTTGAAATTTTGGAGCCATTGGGAAAGGCGATTTGGGAGGTCTGCATTGTA 122
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QY 723 ACTGTTGTAACCTTACCTTCTGCTGTTGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTA 782
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QY 303 GACCTCCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCACCTTCAAGGAA 362
Db 301 GACCTCCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCACCTTCAAGGAA 360
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QY 423 CGCATCATTCACAGGGATATGAAGCCTGACATATTTTACTTGACGAACATGGGCACGTG 482
Db 421 CGCATCATTCACAGGGATATGAAGCCTGACATATTTTACTTGACGAACATGGGCACGTG 480
QY 483 CACATCACAGATTTCAACATTTGCTGGATGCTGCGGATGCTGCGGATGCTGCGGATGCTG 542
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QY 963 AAACCTCTACATAAAGAAAAAAGCGTCTGGCAAGAAAGAGGAGGATATGAGGAATGC 1022
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Db 1141 GAACAAACCAAGACCCCAAGGTGAGGATGCTCAGAAATACAACTTGTAA 1191

RESULT 8
AX320936
LOCUS AX320936 1191 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0181589.
ACCESSION AX320936

VERSION AX320936.1 GI:17902482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meyers, R. and Hunter, J. J.
TITLE 14911 novel protein kinase molecules and uses therefor
JOURNAL Patent: WO 0181589-A 3 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1.1191
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 79.8%; Score 1184.6; DB 6; Length 1191;
Best Local Similarity 99.7%; Pred. No. 2.1e-285;
Matches 1187; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 ATGGGAGCGAACACTTCAAGAAACACCAACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAACACTTCAAGAAACACCAACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60
QY 63 GACCACTTTGAAATTTTGGAGGACCTTGGAAAGGAGTGTGCGAGGCTCTGCATTGTA 122
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QY 423 CGCATCATTCACAGGGATATGAAGCCTGACATATTTTACTTGACGAACATGGGCACGTG 482
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QY 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGAGTGAAGGATATGAAGTCCAGAACAGGAGC 662
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QY 663 AGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGATGAAATGAAGATGTCA 722
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RESULT 9
AR393904
LOCUS AR393904 1675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6617147.
ACCESSION AR393904
VERSION AR393904.1 GI:40121081
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1675)
AUTHORS Hu, Y., Nepomichy, B., Wang, X. and Donoho, G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 12 09-SEP-2003;
FEATURES
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1. .1675
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 78.3%; Score 1162.6; DB 6; Length 1675;
Best Local Similarity 98.8%; Pred. No. 6.9e-240;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Db 411 CCATGGGAGCGAACACTTCAAGAAAAACCAGAGTGTGATGAAATGAAGATGTCAACT 470
QY 61 TTGACCACCTTGAATTTTGGAGGCCATTGGGAAAGGCGAGTTTGGGAGGCTCTGCATTG 120
Db 471 TTGACCACCTTGAATTTTGGAGGCCATTGGGAAAGGCGAGTTTGGGAGGCTCTGCATTG 530
QY 121 TACAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCG 180
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QY 421 AGCGCATCATTCACAGGATATGAAGCCTGACATATTTTACCTTGAACGAACTGGGACG 480
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QY 481 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTAACCA 540
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RESULT 10
AX303187
LOCUS AX303187 1675 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 12 from Patent WO0181557.
ACCESSION AX303187
VERSION AX303187.1 GI:17383669
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS Hu,Y., Nepomnichy,B., Wang,X., Donoho,G., Scoville,J. and Walke,D.W.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0181557-A 12 01-NOV-2001;
Lexicon Genetics Incorporated (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 78.3%; Score 1162.6; DB 6; Length 1675;
Best Local Similarity 98.8%; Pred. No. 6.9e-280;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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RESULT 11
AR393902
LOCUS AR393902 1224 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6617147.
ACCESSION AR393902
VERSION AR393902.1 GI:40121077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1224)
AUTHORS Hu,Y., Nepomnichy,B., Wang,X. and Donoho,G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 8 09-SEP-2003;
FEATURES Location/Qualifiers
source 1. .1224
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 78.2%; Score 1160.6; DB 6; Length 1224;
Best Local Similarity 98.8%; Pred. No. 2.2e-279;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 3 ATGGGAGCGAACACTTCAAGAAAACACCACAGTGTGTTGATGAAAATGAAGATGTCAACTTT 62
Db 1 ATGGGAGCGAACACTTCAAGAAAACACCACAGTGTGTTGATGAAAATGAAGATGTCAACTTT 60
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Qy 1143 GAACAAACCAAGACCCCAAGGTGAGGATGGTCAGAATAACA 1185
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RESULT 13
AX833107
LOCUS AX833107 2063 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 231 from Patent EP1347046.
ACCESSION AX833107
VERSION AX833107.1 GI:39919242
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 231 24-SEP-2003;
Research Association for Biotechnology (JRP)
FEATURES
source 1. .2063
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 69.3%; Score 1029.4; DB 6; Length 2063;
Best Local Similarity 99.4%; Pred. No. 1.5e-246;
Matches 1033; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGATGAAAAATGAAGATGTCAACT 60
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Db 812 TGCACATCACAGATTTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACA 871
Qy 541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCT 600
Db 872 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCT 931
Qy 601 ATTCTTTTGTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCC 660
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RESULT 14
AK094580
LOCUS AK094580 2063 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ37261 fis, clone BRAMY2010464, moderately similar to Mus musculus mRNA for serine/threonine protein kinase.
ACCESSION AK094580
VERSION AK094580.1 GI:21753667
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
TITLE Unpublished

REFERENCE 2 (bases 1 to 2063)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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/db_xref="taxon:9606"
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/clone_lib="BRAMY2"
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Best Local Similarity 99.4%; Pred. No. 1.5e-246;
Matches 1033; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 452 TACAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGG 511
QY 181 TGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCAGGCTTGGAGC 240
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DB 632 TGACCTCTCTGCTGGTGGAGACCTGCTGTTATCACCTGCAACAGAACGTCCTCAAGG 691
QY 361 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGCGCCTGGACTACCTGCAGAAC 420
DB 692 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGCGCCTGGACTACCTGCAGAAC 751
QY 421 AGCGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACG 480
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QY 481 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCA 540
DB 812 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCA 871
QY 541 TGGCTGGACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAGGAGCAGGCT 600
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QY 601 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATGCTGAGAGGCC 660
DB 932 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATGCTGAGAGGCC 991

QY 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGTGAGA 720
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QY 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840
DB 1112 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 1171
QY 841 ATATGAATGATATAAAGCTGGGATGAGTTTTCAGAAAGAGGCTCATTCAGAGTTTCATTC 900
DB 1172 ATATGAATGATATAAAGCTGGGATGAGTTTTCAGAAAGAGGCTCATTCAGAGTTTCATTC 1231
QY 901 CTAATAAAGGAGGCTGAATTTGTGATCTCTACCTTTGAACTTGAGGAAATGATTTGGAGT 960
DB 1232 CTAATAAAGGAGGCTGAATTTGTGATCTCTACCTTTGAACTTGAGGAAATGATTTGGAGT 1291
QY 961 CCAAACTCTACATAAAGAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1020
DB 1292 CCAAACTCTACATAAAGAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1351
QY 1021 GCGATTCTTCTCAGACATG 1039
DB 1352 GCGATTCTTCTCAGGTAAG 1370
RESULT 15
AX166513
LOCUS AX166513 981 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4 from Patent WO0138503.
ACCESSION AX166513
VERSION AX166513.1 GI:14546858
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Planagan,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 4 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 90.7%; Pred. No. 5.1e-197;
Matches 903; Conservative 0; Mismatches 78; Indels 15; Gaps 1;
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DB 1 ATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGATGAAAAATGAAGATGTCAACTTT 60
QY 63 GACCACCTTTGAAATTTTGGAGGCAATTTGGGAAAGGCAGTTTGGGGAGGCTGTCATTGTA 122
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QY 123 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAGAGTGGCGT 182
DB 121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGCGT 180
QY 183 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGCAGGCTTGGAGCAC 242
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QY 243 CCTTCTCTGGTTAATTTGTTGGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTGGTG 302
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 241 CCTTCTCTGGTTAATTTGTTGGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTGGTG 300
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 301 GACCTCTCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCTTCAAGGAA 360
 QY 363 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGCTGCAAGAACATGCGGCAAGTG 422
 Db |||||
 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGCTGCAAGAACATGCGGCAAGTG 420
 QY 423 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGAAGAACATGCGGCAAGTG 482
 Db |||||
 421 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGAAGAACATGCGGCAAGTG 480
 QY 483 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 542
 Db |||||
 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG 540
 QY 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAGGAGCAGGCTAT 602
 Db |||||
 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAGGAGCAGGCTAT 600
 QY 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCCGG 662
 Db |||||
 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGGCCGG 660
 QY 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATGTACACACGTTTGAGACG 722
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 QY 723 ACTGTTGTAACCTTACCCCTTCTGCTGGTCCAGGAAATGTTGCTTCTTAAAAAGCTA 782
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 781 AGAAGGAAGACTGCATGTC-----CAAACGAAGTAACAAAGGAAGCAGG 825
 QY 843 ATGAATGATATAAACTGGGATGCAAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 902
 Db |||||
 826 CTCTCTGGCTTAAGTTTAGAAGTTAGTATACAAATATTGGGGACACCAACTGTCTTCTCTTG 885
 QY 903 AATAAAGGCGGCTGAATTTGATCCTTACCTTTGAACTTGAGGAATGATTTTGGAGTCC 962
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 886 CAGAAAGGCGGCTGAATTTGATCCTTACCTTTGAACTTGAGGAATGATTTTGGAGTCC 945
 QY 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAAG 998
 Db |||||
 946 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAAG 981

Search completed: June 26, 2004, 22:20:15
 Job time : 4053 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:47:04 ; Search time 44 Seconds
(without alignments)
2839.664 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFDEVEDVNF.....NLALEQTKDPQGEDGQNNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1899	90.3	398	11 Q8BGW6	Q8bgw6 mus musculus
2	1726	82.0	368	11 Q7TPQ4	Q7tpq4 mus musculus
3	1438.5	68.4	414	11 Q7TMD3	Q7tmd3 mus musculus
4	1437.5	68.3	414	11 Q9JUX8	Q9jjx8 mus musculus
5	1434.5	68.2	414	11 Q8C4E0	Q8c4e0 mus musculus
6	1425.5	67.8	414	4 Q9NY57	Q9ny57 homo sapien
7	1421.5	67.6	414	4 Q8IY14	Q8iy14 homo sapien
8	1324	62.9	486	4 Q86UX6	Q86ux6 homo sapien
9	1317.5	62.6	488	11 Q9JUG4	Q9jjg4 mus musculus
10	1317.5	62.6	488	11 Q8QZV4	Q8qzv4 mus musculus
11	1137.5	54.1	369	4 Q96BA3	Q96ba3 homo sapien
12	1137.5	54.1	369	4 Q86UE1	Q86ue1 homo sapien
13	1122.5	53.4	368	6 Q9BGT4	Q9bgt4 macaca fasc
14	843.5	40.1	379	5 Q21483	Q21483 caenorhabdi
15	822	39.1	166	4 Q8WU08	Q8wu08 homo sapien
16	711.5	33.8	700	5 Q9VN23	Q9vn23 drosophila

17	675	32.1	367	3 Q96WJ8	Q96wj8 blumeria gr
18	548.5	26.1	735	5 Q8I4W3	Q8i4w3 plasmodium
19	521	24.8	480	10 Q43380	Q43380 avena sativ
20	516	24.5	456	5 Q8MYF1	Q8myf1 dictyosteli
21	515.5	24.5	648	5 Q9TXB8	Q9txb8 dictyosteli
22	514.5	24.5	465	10 Q8LFC1	Q8lfc1 arabidopsis
23	513.5	24.4	352	5 Q25115	Q25115 hemicentrot
24	512.5	24.4	522	3 Q9Y777	Q9y777 metarhizium
25	512	24.3	462	5 Q97116	Q97116 amblyomma a
26	508.5	24.2	421	5 Q97115	Q97115 amblyomma a
27	508	24.1	371	5 Q97114	Q97114 amblyomma a
28	507.5	24.1	530	3 Q42793	Q42793 colletotric
29	507.5	24.1	919	3 Q8NIK8	Q8nik8 emericella
30	507	24.1	352	5 Q16957	Q16957 aplysia cal
31	506.5	24.1	772	5 Q18846	Q18846 caenorhabdi
32	506.5	24.1	917	3 Q9HGS0	Q9hgs0 botrytis ci
33	504.5	24.0	536	3 Q9P466	Q9p466 neurospora
34	502.5	23.9	502	3 Q8J129	Q8j129 aspergillus
35	501.5	23.8	726	4 Q7Z3Z7	Q7z3z7 homo sapien
36	501.5	23.8	726	6 Q7YQL2	Q7yql2 pan troglod
37	501.5	23.8	726	6 Q7YQL1	Q7yql1 pongo pygma
38	501.5	23.8	758	6 Q9BE29	Q9be29 macaca fasc
39	501	23.8	360	5 Q16933	Q16933 ancylostoma
40	500.5	23.8	351	13 Q90WN3	Q90wn3 xenopus lae
41	500.5	23.8	490	3 Q96UM3	Q96um3 aspergillus
42	500.5	23.8	733	4 Q96J38	Q96j38 homo sapien
43	499.5	23.7	587	4 Q8WM06	Q8wm06 homo sapien
44	498.5	23.7	343	6 Q9MZD8	Q9mzd8 ovis aries
45	498.5	23.7	539	3 Q01143	Q01143 magnaporthe

ALIGNMENTS

RESULT 1

Q8BGW6 ID Q8BGW6 PRELIMINARY; PRT; 398 AA.
AC Q8BGW6;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to serine threonine kinase 32 homolog.
GN A930015B13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK036266; BAC29366.1; -.
DR EMBL; AK042599; BAC31302.1; -.
DR EMBL; AK044474; BAC31941.1; -.
DR MGI; MGI:2442403; A930015B13RIK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6;
Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC052404; AAH52404.1; -;
EMBL; BC056396; AAH56396.1; -;
Hypothetical protein.
SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;

Query Match 68.4%; Score 1438.5; DB 11; Length 414;
Best Local Similarity 68.5%; Pred. No. 8.1e-112;
Matches 280; Conservative 39; Mismatches 71; Indels 19; Gaps 4;

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DB 1 MGGNHSKPPVFDENEVNFDFHFEILRAIGKSGFGEVCIVQNDTKKCMKYMKNQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
DB 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120

QY 121 ETVKLFICELVMDYLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIITM 180
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QY 239 ETTVTYTPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGF 298
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QY 358 EPIIFNREKVRNDRFNKQPNLALEQTKDPQG-----EDGQNNNL 396
DB 361 EPIIFNREKLRQOQHN-----GQLSLDGRIGSQTSKQLQDGRNNNI 403

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AC Q9JJX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN STK32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,

Goodship J.;
"Mutations in a new gene in Ellis-van creveld syndrome and Weyers
acrodental dysostosis.";
Nat. Genet. 24:283-286 (2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ250840; CAB76566.1; -;
DR HSSP; P05132; ICTP.
DR MGD; MGI:1927552; Stk32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;

Query Match 68.3%; Score 1437.5; DB 11; Length 414;
Best Local Similarity 69.7%; Pred. No. 9.8e-112;
Matches 278; Conservative 38; Mismatches 64; Indels 19; Gaps 3;

QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQNDTKKCMKYMKNQKCV 60
DB 1 MGGNHSKPPVFDENEVNFDFHFEILRAIGKSGFGEVCIVQNDTKKCMKYMKNQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
DB 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120

QY 121 ETVKLFICELVMDYLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIITM 180
DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVLKSEKASSM 180

QY 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTE 238
DB 181 AGTKPYMAPEVQVYVDGGPGYSYPVDWWSLGVATAYELLRGRPPYHRSATPIDEILNMF 240

QY 239 ETTVTYTPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSWCEGMVSLKLLTKDPESLSSLRDIQSMYTLADNMWDVAFKALMPGF 300

QY 299 IPNKGRLNCDPTFELEEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRSDTKDSCPLNGHLQOCLETVRK 360

QY 358 EPIIFNREKVRNDRFNKQPNLALEQTKDPQG-----EDGQNNNL 396
DB 361 EPIIFNREKLRQOQHN-----GQLSLDGRIGSQTSKQLQDGRNNNI 403

RESULT 5
Q8C4E0 PRELIMINARY; PRT; 414 AA.
AC Q8C4E0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine threonine kinase 32.
GN STK32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK082468; BAC38500.1; --.
DR MGD; MGI:1927552; Stk32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;

Query Match 68.2%; Score 1434.5; DB 11; Length 414;
Best Local Similarity 68.2%; Pred. No. 1.7e-111;
Matches 279; Conservative 40; Mismatches 71; Indels 19; Gaps 4;

QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCAMKYMKNQKCV 60
Db 1 MGNHSHKPPVFDENEVNFDFHFEILRAIGKSGFGKVCIVQKRDTKKMYAMKYMKNQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120

QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFTNIAAMLPRETQITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFTNIAATVKGSEKASSV 180

QY 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVFQVYVGGPGYSYPVDWWSLGVATAYELLRGRWPYEHISATPIDEILNMF 240

QY 239 ETTVTYTPSAWSQEMVSLKKLLPNPDQFSQLSDVQNFPPYNDINWDVAFQKRLIPGF 298
Db 241 KVERVHYSSTWCGMVSLLKKLLTKOPESRLSLRDIQSMTYLADNMWDVAFKALMPGF 300

QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKMRKCDSSQTCLLQEHLDVQK 357
Db 301 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRDSSTKOSCPNLGHLQCCLETVRK 360

QY 358 EPIIFNREKVNDRFNKQPNLALAEQTKDPQG-----EDQNNNL 396
Db 361 EPIIFNREKLRQOQHN-----GQLSDLDGRIGSQTSKQLQDGRNNNI 403

RESULT 6
Q9NY57
ID Q9NY57 PRELIMINARY; PRT; 414 AA.
AC Q9NY57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrodermal dysostosis.";
RL Nat. Genet. 24:283-286(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ250839; CAB76471.1; --.
DR HSSP; P05132; ICTP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47883 MW; 8FCD58A67EF09B0E CRC64;

Query Match 67.8%; Score 1425.5; DB 4; Length 414;
Best Local Similarity 68.2%; Pred. No. 9.9e-111;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCAMKYMKNQKCV 60
Db 1 MGNHSHKPPVFDENEVNFDFHFEILRAIGKSGFGKVCIVQKRDTKKMYAMKYMKNQKCI 60

QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120

QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFTNIAAMLPRETQITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFTNIAATVVGAEARASSM 180

QY 181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVFQVYVMDRGPYSPVDWWSLGVATAYELLRGRWPYEHISATPIDEILNMF 240

QY 239 ETTVTYTPSAWSQEMVSLKKLLPNPDQFSQLSDVQNFPPYNDINWDVAFQKRLIPGF 298
Db 241 KVERVHYSSTWCGMVSLLKKLLTKDPESRVSSLDHDIQSVPYLADNMWDVAFKALMPGF 300

QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKMRKCDSSQTCLLQEHLDVQK 357
Db 301 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRDSSTKOSCPNLGHLQCCLETVRE 360

QY 358 EPIIFNREKVNDRFNKQPNLALAEQTKDPQG---EDQNNNL 396
Db 361 EPIIFNREKLRQOQGSQQLDTSRGGGQAQSKLQDGCNNNL 403

RESULT 7
Q8IY14
ID Q8IY14 PRELIMINARY; PRT; 414 AA.
AC Q8IY14;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gene for serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038238; AAR38238.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 414 AA; 47784 MW; F0E5EE6595FA8242F CRC64;

Query Match 67.6%; Score 1421.5; DB 4; Length 414;
Best Local Similarity 68.2%; Pred. No. 2.1e-110;
Matches 275; Conservative 43; Mismatches 78; Indels 7; Gaps 3;

QY 1 MGANTSRKPPVDFENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60
Db 1 MGNHSHKPPVDFENEVNFDFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120
Db 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVVKGAERASM 180
QY 181 AGTKPYMAPEMFSS--SRKGAGYSFVDWWSLGVTAAYELLRGRPRPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVQVYMDGGPGYSYPVDWWSLGITAYELLRGRWPYHRSVTPIDEILNMF 240
QY 239 ETTVVTPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGF 298
Db 241 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLDHDIQSVPYLADNMWDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKMRKCDSSQTCLLQEHLDVQK 357
Db 301 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSDRGTKDSCPLNGHLQHCLETRE 360
QY 358 EPIIFNREKVRNDFNKRQPNLALEQTDPQG----EDGQNNNL 396
Db 361 EPIIFNREKVRNDFNKRQPNLALEQTDPQG--KRSQDLPREPLPAPESRD 403

RESULT 8
Q86UX6 PRELIMINARY; PRT; 486 AA.
AC Q86UX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PKE protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma A.-H.; Nelson D.A.; Xia L.; Ravi L.; Chen H.-C.; Robinson D.R.;
RA Kung H.-J.;
RT "PKE, A New Human AGC Group Kinase, Phosphorylates SET, a PP2A

RT Inhibitor."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY098866; AAM21719.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 486 AA; 54994 MW; 38FEFBB3863B21F3 CRC64;

Query Match 62.9%; Score 1324; DB 4; Length 486;
Best Local Similarity 64.5%; Pred. No. 3.7e-102;
Matches 254; Conservative 53; Mismatches 77; Indels 10; Gaps 4;

QY 1 MGANTSRKPPVDFENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60
Db 72 MSAATARR--PVFDDKEDVNFDFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCI 130
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120
Db 131 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVQFSE 190
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
Db 191 DTVLYICELMALDYLGRGQIIHRDVKPDNILLDERGHAHLTDFNIAATIKOGERATAL 250
QY 181 AGTKPYMAPEMFSS--RKGAGYSFVDWWSLGVTAAYELLRGRPRPYHRSSTSSKEIVHTF 238
Db 251 AGTKPYMAPEIFHFSFVNGGTGYSFVDWWSVGMAYELLRGRWPYDIHSSNAVESLVQLF 310
QY 239 ETTVVTPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGF 298
Db 311 STSVSVQYVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVLWDHLSKRVPEPGF 370
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAKKEKMRKCDSSQT--CLLQEHLDVQ 356
Db 371 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSDSSQSENLYQDCLDAIQ 430
QY 357 KEPIIFNREKVRNDFNKRQPNLALEQTDPQGED 390
Db 431 QDFVIFNREKL-----KRSQDLPREPLPAPESRD 459

RESULT 9
Q9JJG4 PRELIMINARY; PRT; 488 AA.
AC Q9JJG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain cDNA, clone MNCb-1563, similar to AJ250840 serine/threonine
DE protein kinase (Mus musculus).
DE PKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N.; Kusuda J.; Tanuma R.; Ito A.; Hirata M.; Sugano S.;
RA Hashimoto K.;

RT "Isolation of full-length cDNA clones from mouse brain cDNA library
made by oligo-capping method."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB041542; BAA95027.1; -.
DR HSSP; P05132; 1CTP.
DR MGD; MGI:2385336; Pke.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55276 MW; 310483FF69E24E39 CRC64;

Query Match 62.6%; Score 1317.5; DB 11; Length 488;
Best Local Similarity 64.3%; Pred. No. 1.3e-101;
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;
QY 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKMKAMKYNKQKVERNEV 65
Db 77 SARRPVDDKEDVNFDFHFIQLRAIGKSGFGKVCIVQKRDTEKVMYKYNKQCIERDEV 136
QY 66 RNVFKEIQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKETVKL 125
Db 137 RNVERLEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVQFSEDIVRL 196
QY 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 185
Db 197 YICEMALALDYLRSHQIHRDVKPDNILLDEQGHVHITDFNIAATIKDGERATALAGTKP 256
QY 186 YMAPEMFSS--RKGAGYSFVADWWSLGVATAYELLRGRPRPYHIRSTSSKEIVHTFTTV 243
Db 257 YMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGRWPRPYDIHSSNAVESLVQLFSTVS 316
QY 244 TYPYSAWSQEMVSLKLLLEPNPDQRFSLSDVQNFYNDINWDVAFQKRLIPGIPNKG 303
Db 317 QYVPTWSKEMVALLRKLTVNPEHRFSLQDMQTAPSLAHVLDLSEKKVEPGFVFNKG 376
QY 304 RLNCDPPTFELEEMILESRLHKKKKRLAKCKEKMRCDCSSQT--CLLQEHLDVQKEFI 361
Db 377 RLHCDPTFELEEMILESRLHKKKKRLAKCKEKMRCDCSSQSENQDYLDCLDAIQQDFVI 436
QY 362 FNREKVNDRFNKQPNLALQTKDPQGED 390
Db 437 FNREKL-----KRSQELMSEPPPGPETS 460

RESULT 10
Q8QZV4
ID Q8QZV4 PRELIMINARY; PRT; 488 AA.
AC Q8QZV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical serine/threonine protein kinase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC026457; AAH26457.1; -.
DR EMBL; AK046439; BAC32730.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55262 MW; 2B6A927BE6B78EF2 CRC64;

Query Match 62.6%; Score 1317.5; DB 11; Length 488;
Best Local Similarity 64.3%; Pred. No. 1.3e-101;
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;
QY 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKMKAMKYNKQKVERNEV 65
Db 77 SARRPVDDKEDVNFDFHFIQLRAIGKSGFGKVCIVQKRDTEKVMYKYNKQCIERDEV 136
QY 66 RNVFKEIQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKETVKL 125
Db 137 RNVERLEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVQFSEDIVRL 196
QY 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 185
Db 197 YICEMALALDYLRSHQIHRDVKPDNILLDEQGHVHITDFNIAATIKDGERATALAGTKP 256
QY 186 YMAPEMFSS--RKGAGYSFVADWWSLGVATAYELLRGRPRPYHIRSTSSKEIVHTFTTV 243
Db 257 YMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGRWPRPYDIHSSNAVESLVQLFSTVS 316
QY 244 TYPYSAWSQEMVSLKLLLEPNPDQRFSLSDVQNFYNDINWDVAFQKRLIPGIPNKG 303
Db 317 QYVPTWSKEMVALLRKLTVNPEHRFSLQDMQTAPSLAHVLDLSEKKVEPGFVFNKG 376
QY 304 RLNCDPPTFELEEMILESRLHKKKKRLAKCKEKMRCDCSSQT--CLLQEHLDVQKEFI 361
Db 377 RLHCDPTFELEEMILESRLHKKKKRLAKCKEKMRCDCSSQSENQDYLDCLDAIQQDFVI 436
QY 362 FNREKVNDRFNKQPNLALQTKDPQGED 390
Db 437 FNREKL-----KRSQELMSEPPPGPETS 460

RESULT 11
Q96BA3
ID Q96BA3 PRELIMINARY; PRT; 369 AA.
AC Q96BA3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC015792; AAH15792.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42425 MW; 83C54C4AF7D792E5 CRC64;

Query Match 54.1%; Score 1137.5; DB 4; Length 369;
Best Local Similarity 62.8%; Pred. No. 9.9e-87;
Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;

QY 48 MCAMKYNKQKVERNEVRNFKELQIMQGLEHPLVNLWYSFQDEDMFMVVDLLGGD 107
Db 1 MYAMKYNKQKQCIERDEVRNFRLEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60

QY 108 LRYHLQONVHFKEETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNI 167
Db 61 LRYHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120

QY 168 AAMPLPRETQITTMAGTKPYMAPEMFSS--RKAGYSFAVDWWSLGVYAYELLRGRPYHI 225
Db 121 ATIIKQGERATAGTKPYMAPEMFHFSFVNGTGYSEFVDWWSVGMAYELLRGRPYDI 180

QY 226 RSSTSSKEIVHTFETTVTPYSAWSQEMVSLKLLLEPNPDQRFSLSDVQNFPPYMDIN 285
Db 181 HSSNAVESLVQLFSTVSQVYVPTWSKEMVALLRKLTVNPEHRLSLSDVQAAPALAGVL 240

QY 286 WDAVFQKRLIPGFIIPKGRNLCDPTFELEEMILESKPLHKKRKLAKKDKMRKCDSSQT 345
Db 241 WDHLSEKRVPEPGFVFNKGRHLCDPTFELEEMILESRPLHKKRKLAKKDKMRKCDSSQT 300

QY 346 --CLLQEHLDVQKBEFIIFNREKVRNDFNKRQPNLALALEQTKDPQGED 390
Db 301 ENDYLQDCLDAIQQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342

RESULT 12
Q86UE1 PRELIMINARY; PRT; 369 AA.
AC Q86UE1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PKC protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045760; AAH45760.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 369 AA; 42395 MW; E152C66BB2D786B4 CRC64;

Query Match 54.1%; Score 1137.5; DB 4; Length 369;
Best Local Similarity 62.8%; Pred. No. 9.9e-87;
Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;

QY 48 MCAMKYNKQKVERNEVRNFKELQIMQGLEHPLVNLWYSFQDEDMFMVVDLLGGD 107
Db 1 MYAMKYNKQKQCIERDEVRNFRLEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60

QY 108 LRYHLQONVHFKEETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNI 167
Db 61 LRYHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120

QY 168 AAMPLPRETQITTMAGTKPYMAPEMFSS--RKAGYSFAVDWWSLGVYAYELLRGRPYHI 225
Db 121 ATIIKQGERATAGTKPYMAPEMFHFSFVNGTGYSEFVDWWSVGMAYELLRGRPYDI 180

QY 226 RSSTSSKEIVHTFETTVTPYSAWSQEMVSLKLLLEPNPDQRFSLSDVQNFPPYMDIN 285
Db 181 HSSNAVESLVQLFSTVSQVYVPTWSKEMVALLRKLTVNPEHRLSLSDVQAAPALAGVL 240

QY 286 WDAVFQKRLIPGFIIPKGRNLCDPTFELEEMILESKPLHKKRKLAKKDKMRKCDSSQT 345
Db 241 WDHLSEKRVPEPGFVFNKGRHLCDPTFELEEMILESRPLHKKRKLAKKDKMRKCDSSQT 300

QY 346 --CLLQEHLDVQKBEFIIFNREKVRNDFNKRQPNLALALEQTKDPQGED 390
Db 301 ENDYLQDCLDAIQQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342

RESULT 13
Q9BGT4 PRELIMINARY; PRT; 368 AA.
ID Q9BGT4
AC Q9BGT4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Frontal cortex;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB056389; BAB33045.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; ATP-binding; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DABCC14 CRC64;
 Query Match 53.4%; Score 1122.5; DB 6; Length 368;
 Best Local Similarity 62.8%; Pred. No. 1.8e-85;
 Matches 218; Conservative 44; Mismatches 76; Indels 9; Gaps 3;
 QY 48 MCAMKYNKQKVERNEVRNFKELQIMQGLEHPELVNLYSFDDEDMFMVVDLLGGD 107
 DB 1 MYAMKYNKQQCIEDEVRNVRNFKELQIEHVFVNLYSFDDEDMFMVVDLLGGD 60
 QY 108 LRYHLQNVHFKEETVKLFICELVMDLYLQNRRIHHRMKNPDNILLDEHGHVHTDFNI 167
 DB 61 LRYHLQNVQFSEDTVRLYICEMALDYLQCGHIIHHRMKNPDNILLDERGHAHLTDFNI 120
 QY 168 AAMLPRETQITTMAGTKPYMAPENFSS--RKGAGYSFVDWWSLGVATYELLRGRPYHI 225
 DB 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVATYELLRGRPYDI 180
 QY 226 RSSTSSKEIVHTFETTVVTPYSAWSQEMVSLKGLLEPNPDQFSLSDVQNFPMNDIN 285
 DB 181 HSSNAVESLVQLFSTVSQYVPTWSREVMVALLRLKLTVNPEHRSFSLQDVQAAPALAGVL 240
 QY 286 WDAVFOKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKRLAKKEMKCDSSQT 345
 DB 241 WGHLSKREVEPDPVFNKGRHLNCDPTFELEEMILESRPLHKKKRLAKKNSRDNSRDSQS 300
 QY 346 --CLLQEHLDVQKEPIIFNREKVNDRDNKQPNLALEQTKDQGED 390
 DB 301 ENDYLDCLDAIQDQFVIFNREKL-----KRSQDLPEPLPAPEPRD 342
 RESULT 14
 Q21483
 ID Q21483 PRELIMINARY; PRT; 379 AA.
 AC Q21483;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE M03C11.1 protein.
 GN M03C11.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RA McMurray A.A.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology";
 RL Science 282:2012-2018(1998).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; Z49128; CAA88953.1; -.
 DR PIR; T23688; T23688.
 DR HSSP; Q63450; LA06.
 DR WormPep; M03C11.1; CE03492.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 379 AA; 43632 MW; 5E2090A15812D27D CRC64;
 Query Match 40.1%; Score 843.5; DB 5; Length 379;
 Best Local Similarity 44.1%; Pred. No. 3.8e-62;
 Matches 158; Conservative 70; Mismatches 117; Indels 13; Gaps 4;
 QY 22 HFEILRAIGKSGFGEVCIVQKNDTKKCMAMKYNKQKVERNEVRNFKELQIMQGLEHP 81
 DB 27 HFSVIRSIGRGAFGKVCIVQERKTKKYPALKYNNKRCIEKGAANVIRELTLLSKMSHP 86
 QY 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFKEETVKLFICELVMDLYLQNR 141
 DB 87 FIVNLWYTFQGDYMYMVSDLLGGDLRYHLQNVHFKEETVKLFICELVMDLYLQNR 146
 QY 142 IHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTMAGTKPYMAPENFSS--RKGAG 199
 DB 147 IVHRDIKPNILLDEGHVHTDFNIAAMLPRETQITTMAGTKPYMAPENFSS--RKGAG 206
 QY 200 YSPAVDWWSLGVATYELLRGRPYHRSSTSSKEIVHTFETTVVTPYSAWSQEMVSLK 259
 DB 207 YDSRVDWWSLGVATYELLRGRPYHRSSTSSKEIVHTFETTVVTPYSAWSQEMVSLK 266
 QY 260 LLEPNPDQFSLSDVQNFPMNDINWDAVFOKRLIPGFIPNKGRLNCDPTFELEEMILE 319
 DB 267 MLKFDKXKRLVGLAIAKKHSYTERIDFKSVFEKPSVPIPCKEGLNCDPTFELEERILV 326
 QY 320 SKPLHKKKRLAKKEMKCDSSQTCLLQEHLDVQKEPIIFNREKVNDRDNKQPN 377
 DB 327 STPIH--RRRTNHNSSGRSSSEPQNAALVE---VSKAFIDFSRHNV-----KIEPN 373
 RESULT 15
 Q8WU08
 ID Q8WU08 PRELIMINARY; PRT; 166 AA.
 AC Q8WU08;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to serine threonine kinase 32.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Search completed: June 25, 2004, 10:51:07
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:43:09 ; Search time 18 Seconds
(without alignments)
1145.543 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLALEQTKDPQGEDGQNNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582.5	27.7	444	1 KRAC_DICDI	P54644 dictyosteli
2	537	25.5	479	1 PK2_DICDI	P28178 dictyosteli
3	528.5	25.1	648	1 KAPC_DICDI	P34099 dictyosteli
4	519	24.7	471	1 KP19_ARATH	Q39030 arabidopsis
5	516.5	24.5	465	1 KPK1_ARATH	P42818 arabidopsis
6	513	24.4	680	1 YPK1_YEAST	P12688 saccharomyc
7	511.5	24.3	696	1 SCK1_SCHPO	P50530 schizosacch
8	510.5	24.3	352	1 KAPC_DROME	P12370 drosophila
9	503	23.9	404	1 KAPC_CAEEL	P21137 caenorhabdi
10	502.5	23.9	350	1 KAPA_CRIGR	P25321 cricetulus
11	502.5	23.9	350	1 KAPA_PIG	P36887 sus scrofa
12	502.5	23.9	823	1 SCH9_YEAST	P11792 saccharomyc
13	501.5	23.8	740	1 K6A3_HUMAN	P51812 homo sapien
14	501.5	23.8	740	1 K6A3_MOUSE	P18654 mus musculu
15	501	23.8	677	1 YPK2_YEAST	P18961 saccharomyc
16	500.5	23.8	350	1 KAPG_HUMAN	P22612 homo sapien
17	500.5	23.8	733	1 K6A2_HUMAN	Q15349 homo sapien
18	498.5	23.7	349	1 KAPA_CANFA	Q8mj44 canis famli
19	498.5	23.7	350	1 KAPA_HUMAN	P17612 homo sapien
20	498.5	23.7	350	1 KAPA_RAT	P27791 rattus norv
21	498.5	23.7	350	1 KAPA_SHEEP	Q9mzd9 ovis aries
22	498.5	23.7	689	1 ARK1_HUMAN	P25098 homo sapien
23	496.5	23.6	350	1 KAPA_BOVIN	P00517 bos taurus
24	496.5	23.6	733	1 K6A2_MOUSE	Q9wut3 m ribosomal
25	496	23.6	350	1 KAPB_MOUSE	P05206 mus musculu
26	495.5	23.6	586	1 KPCI_MOUSE	Q62074 mus musculu
27	495.5	23.6	587	1 KPCI_HUMAN	P41743 homo sapien
28	494.5	23.5	752	1 K6AA_CHICK	P18652 gallus gall
29	493.5	23.5	398	1 KAPC_YEAST	P05986 saccharomyc
30	493.5	23.5	646	1 KDBE_SCHPO	Q10364 schizosacch
31	493.5	23.5	689	1 ARK1_BOVIN	P21146 bos taurus
32	493	23.4	689	1 ARK1_MESAU	Q64682 mesocricetu
33	492.5	23.4	350	1 KAPA_MOUSE	P05132 mus musculu

RESULT 1

ID	KRAC_DICDI	STANDARD;	PRT;	444 AA.
AC	P54644;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	RAC-family serine/threonine kinase homolog (EC 2.7.1.-).			
GN	PKBA OR DAGA.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AX3;			
RA	Moon B., Haribabu B., Rabino M., Ortiz B., Reichel G., Skehel P., Williams J., Bouzid S., Veron M., Dottin R.P.; Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.			
RL	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC			
CC	SUBFAMILY. STRONGEST TO YEAST YPK1/YPK2.			
CC	-!- SIMILARITY: Contains 1 PH domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U15210; AAA76692.1; -.			
DR	HSSP; P05132; ICTP.			
DR	DictyBase; DDB0003794; pkba.			
DR	InterPro; IPR001849; PH.			
DR	InterPro; IPR000961; Pkinase C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	Pfam; PF00169; PH; 1.			
DR	Pfam; PF00069; pkinase; 1.			
DR	Pfam; PF00433; pkinase C; 1.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00233; PH; 1.			
DR	SMART; SM00133; S_TK_X; 1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00003; PH DOMAIN; 1.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.			
FT	DOMAIN 5 100 PH.			
FT	DOMAIN 120 374 PROTEIN KINASE.			
FT	NP BIND 126 134 ATP (BY SIMILARITY).			
FT	BINDING 149 149 ATP (BY SIMILARITY).			
FT	ACT SITE 243 243 BY SIMILARITY.			
SQ	SEQUENCE 444 AA; 51062 MW; 12367A1A411C5680 CRC64;			

ALIGNMENTS

34	492.5	23.4	689	1 ARK1_RAT	P26817 rattus norv
35	491.5	23.4	733	1 K6AA_XENLA	P10665 xenopus lae
36	490	23.3	512	1 KAPB_SCHPO	P40376 schizosacch
37	488.5	23.2	629	1 K6AB_XENLA	P10666 xenopus lae
38	487.5	23.2	745	1 K6A6_HUMAN	Q9uk32 homo sapien
39	487	23.1	380	1 KAPB_HUMAN	P06245 saccharomyc
40	486.5	23.1	350	1 KAPB_YEAST	P22694 homo sapien
41	486	23.1	350	1 KAPB_BOVIN	P05131 bos taurus
42	486	23.1	397	1 KAPI_BOVIN	P24256 bos taurus
43	485.5	23.1	479	1 AKT3_HUMAN	Q9y243 homo sapien
44	485.5	23.1	479	1 AKT3_MOUSE	Q9wua6 mus musculu
45	485	23.1	350	1 KAPB_PIG	P05383 sus scrofa

thaliana.";
Nature 408:820-822(2000).
[3]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
genome."
Science 302:842-846(2003).
CC -!- FUNCTION: May be involved in adaptation of plant to cold or high-
salt conditions.
CC -!- PTM: Undergoes serine-specific autophosphorylation (By
similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
kinase subfamily.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
frameshift in position 391.

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or send an email to license@isb-sib.ch).

EMBL; D42061; BAA07661.1; --
EMBL; AC012562; AAG51345.1; --
EMBL; AF325094; AAK17162.1; --
EMBL; AY050826; -; NOT_ANNOTATED_CDS.
PIR; S68463; S68463.
HSSP; P05132; 1CTP.
InterPro; IPR000961; Pkinase C.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase C; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
FT DOMAIN 140 395 PROTEIN_KINASE.
FT NP BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT SITE 263 263 BY SIMILARITY.
FT CONFLICT 250 250 A -> V (IN REF. 1).
FT CONFLICT 359 360 LS -> VF (IN REF. 1).
SQ SEQUENCE 471 AA; 53037 MW; 95F007B44B58DFB5 CRC64;

Query Match 24.7%; Score 519; DB 1; Length 471;

Best Local Similarity 34.0%; Pred. No. 2e-28;
Matches 108; Conservative 64; Mismatches 122; Indels 24; Gaps 4;

QY 12 FDENED-----VNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQK 58
Db 116 FSGNDDTDSEKSPBEVSGVVGIEDFEVLKVVGGAGFKVYQVRKQDTSEIYAMKVMRKDK 175
QY 59 CVERNEVRNVFKEIQMQLGHPFLVNLWYSFQDEEDMFVVDLLGLGDLRYHLQONVHF 118
Db 176 IVEKNHAEYMKARDILTKIDHPFIVQLKYSFQTKVRLYLVLDFINGHGLFFQLYHQGLF 235
QY 119 KEETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEGHVHITDFENIAAMLPRETQIT 178
Db 236 REDLARVYTAEIVSAVSHLHEKGIMHRDLKPENILMDVDGHVMLTDFGLAKEFEENTRSN 295
QY 179 TWAGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLRGRPYHIRSSTSSKEIVHTF 238
Db 296 SMCCTTEYMAPEIV---RGKGDKAADWWSVGLLYEMLTGKPPFLGSKGKIQQKIV--- 349
QY 239 ETTVVTYPSAWSQEMVSLKLLKLEPNPDQRF-----SQLSDVQNFPMNDINWDVAFQKRL 294
Db 350 -KDKIKLPOFLSNEAHALLKGLLQKEPERRLGSPSGABEIKKHKWFKAINKWKLEAREV 408
QY 295 IPGFIPNKGRLNCDPTFE 312.
Db 409 QPSFKPAVSGRQCIANFD 426

RESULT 5
KPK1_ARATH STANDARD; PRT; 465 AA.
AC P42818;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Serine/threonine-protein kinase AtPK1/AtPK6 (EC 2.7.1.-).
GN ATPK1 OR ATPK6 OR AT3G08730 OR F17O14.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94292519; PubMed=7912697;
RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
RT "Atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I.
RT Isolation, characterization, and expression."
RL J. Biol. Chem. 269:17586-17592(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95129712; PubMed=7828736;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
RA Shinozaki K.;
RT "Two genes that encode ribosomal-protein S6 kinase homologs are
RT induced by cold or salinity stress in Arabidopsis thaliana."
RL FEBS Lett. 358:199-204(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,


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FT NP BIND 308 316 ATP (BY SIMILARITY).
FT BINDING 331 331 ATP (BY SIMILARITY).
FT ACT_SITE 428 428 BY SIMILARITY.
FT CONFLICT 199 199 A -> R (IN REF. 1).
SQ SEQUENCE 696 AA; 78594 MW; A7B05F5EE4D42AF7 CRC64;

Query Match 24.3%; Score 511.5; DB 1; Length 696;
Best Local Similarity 36.9%; Pred. No. 1e-27;
Matches 111; Conservative 63; Mismatches 112; Indels 15; Gaps 7;

QY 11 VEDENEDVNF--DHFEILRAIGKSGFGEVCIVQKNDTKKCMKYMKNQKQVERNEVRNV 68
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 288 IYEHIEHVRYGPEDEFTALRLIGKGTGQVYLVKNDTRIVAMKKISKKLIVRKKVTHT 347
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 69 FKELQIMQGL--EHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKL 125
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 348 LGERNILVRTSLDESPFIVGLKFSFQTASDLYLITDVMGGELFWHLQHEGRFPQRAKF 407
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIA-AMLPRETQITTMAGTK 184
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 408 YIAELVLALEHLKHDIIVRLKPENILLDADGHIALCDFGLSKANLSANATTNFCGTT 467
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 185 PYMAPEMFSRRKGAGYSFAVDWMSLGVATAYELLRGRPRYHRSSTSSKEIVHTFTTWT 244
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 468 EYLAPEVLLEDK--GYTKQVDFWSLGVLFEMCCGWSPFY--APDVQQMYRNIAPGKVR 522
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 245 YP-SAWSQEMVSLKKLLEPNPDQRFSQLSD---VQNFPMYNDINWDVAFQKRLPGPIP 300
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 523 FPKGVLSSEGRSFVRGLLRNPNHRLGAVADTTTELKEHFFPADINWDLSSKKKQVPPKP 582
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 301 N:301
   |
Db 583 N:583

RESULT 8
KAPC DROME STANDARD; PRT; 352 AA.
AC P12370; Q9VL99;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37) (PKA C).
GN PKA-C1 OR CDKA OR DC0 OR CG4379.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115281; PubMed=2828348;
RA Foster J.L., Higgins G.C., Jackson R.F.;
RT "Cloning, sequence, and expression of the Drosophila CAMP-dependent
RL protein kinase catalytic subunit gene.";
RL J. Biol. Chem. 263:1676-1681(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=89107990; PubMed=3215511;
RA Kalderon D., Rubin G.M.;
RT "Isolation and characterization of Drosophila CAMP-dependent protein
RL kinase genes.";
RL Genes Dev. 2:1539-1556(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- ENZYME REGULATION: Activated by CAMP.
CC -|- SUBUNIT: Composed of two regulatory chains and two catalytic
CC chains.
CC -|- TISSUE SPECIFICITY: More abundant in adult head than adult body.
CC -|- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP
CC subfamily.
CC
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CC
CC -----
CC EMBL; M18655; AAA28412.1; -.
CC EMBL; X16969; CAA34840.1; -.
CC EMBL; AF003625; AAF52797.1; -.
CC FIR; C31751; C31751.
CC HSSP; P05132; 1ATP.
CC FlyBase; FBgn0000273; Pka-C1.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0007448; P:anterior/posterior pattern formation, imagi. .; IMP.
CC GO; GO:0019933; P:CAMP-mediated signaling; NAS.
CC GO; GO:0007456; P:eye morphogenesis (sensu Drosophila); NAS.
CC GO; GO:0007292; P:female gamete generation; IMP.
CC GO; GO:0007611; P:learning and/or memory; NAS.
CC GO; GO:0007480; P:leg morphogenesis (sensu Holometabola); NAS.
CC GO; GO:0045475; P:locomotor rhythm; NAS.
CC GO; GO:0008355; P:olfactory learning; NAS.
CC GO; GO:0007314; P:oocyte anterior/posterior axis determination; IMP.
CC GO; GO:0008103; P:oocyte microtubule cytoskeleton polarization; IMP.
CC GO; GO:0008359; P:regulation of bicoid mRNA localization; IMP.
CC GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz. .; IMP.
CC GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.
CC GO; GO:0007622; P:rhythmic behavior; IMP.
CC GO; GO:0007476; P:wing morphogenesis; IMP.
CC InterPro; IPR000961; Pkinase C.
CC InterPro; IPR000719; Prot_kinase.
```


RT kinase complexed with MgATP and peptide inhibitor.";

RL Biochemistry 32:2154-2161(1993).

CC -!- FUNCTION: Phosphorylates a large number of substrates in the

CC cytoplasm and the nucleus.

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SUBUNIT: A number of inactive tetrameric holoenzymes are produced

CC by the combination of homo- or heterodimers of the different

CC regulatory subunits associated with two catalytic subunits. cAMP

CC causes the dissociation of the inactive holoenzyme into a dimer of

CC regulatory subunits bound to four cAMP and two free monomeric

CC catalytic subunits.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and

CC monomeric catalytic subunit). Translocates into the nucleus

CC (monomeric catalytic subunit) (By similarity).

CC -!- TISSUE SPECIFICITY: Ubiquitously expressed in mammalian tissues.

CC -!- PTM: Asn-2 is deaminated in Asp-2 in more than 25% of the

CC proteins, giving rise to 2 major isoelectric variants, called CB

CC and CA respectively (0.4 pH unit change). Deamidation proceeds via

CC the so-called beta-aspartyl shift mechanism and yields either D-

CC Asp-2 (major) or D-isoAsp-2 (minor), in addition to L-isomers.

CC Deamidation occurs after the addition of myristate. The Asn-2 form

CC reaches a significantly larger nuclear/cytoplasmic ratio than the

CC Asp-2 form.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

CC CAMP subfamily.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X07617; CAA30470.1; --

DR PIR; S00086; S00086.

DR PDB; 1CTP; 31-JAN-94.

DR InterPro; IPR000961; Pkinase_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00433; pkinase_C; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00133; S_TK_X; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW transferase; Serine/threonine-protein kinase; Nuclear protein; cAMP;

KW ATP-binding; Myristate; Phosphorylation; 3D-structure; Lipoprotein.

FT INIT MET 0 0

FT DOMAIN 43 297 PROTEIN KINASE.

FT NP_BIND 49 57 ATP.

FT BINDING 72 72 ATP.

FT ACT_SITE 166 166 BY SIMILARITY.

FT ACT_SITE 199 199 CLOSE TO OR AT THE PEPTIDE SUBSTRATE

FT BINDING SITE.

FT LIPID 1 1 N-myristoyl glycine.

FT MOD_RES 2 2 DEAMIDATION (PARTIAL).

FT MOD_RES 10 10 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 139 139 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 197 197 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 338 338 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 350 AA; 40485 MW; 1C9172E3A3E17B8E CRC64;

Query Match 23.9%; Score 502.5; DB 1; Length 350;

Best local similarity 34.1%; Pred. No. 1.9e-27;

Matches 100; Conservative 75; Mismatches 99; Indels 19; Gaps 6;

QY 19 NFDHFEILRAIGKSGFGEVCIVQKNDTKMKAMKYNKQKCVERNVNFVKELQIMQGL 78

Db 39 HLDQFERIKTLGTSGFGRVMLVGHKETHGNHFAWKILDKQVKVVKLQIEHTLNEKRILQAV 98

QY 79 EHPPLVNLWYSFQDEDMFMVVDLLGLGDLRYHLQNVHFKEETVKLFICELVMALDYIQ 138

Db 99 NFPFLVKLEYSEFKNSNLYMMEYVPGGEMFSLRRIGRSEPHARFYAAQIVLTPEYLH 158

QY 139 NQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSRKA 198

Db 159 SLDLIYRDLKPENLLDQGGYIQVDFGFAKRVKGR--WTLCGTPEYLAPEILSK--- 213

QY 199 GYSFAVDWWSLGVYAYELLGRRRPYHIRSSTSSKEIVHTFETV---VTYPSANQEMVS 255

Db 214 GYNKAVDWWALGVLIYEMAAGYPPFF-----ADQPIYKIVSGKVRFPFSHFSDDKD 267

QY 256 LLKLLLEPNPDQRPSQL---SDVQNFYPMNDINWDVAFQKRLIPGFIPN-KG 303

Db 268 LLRNLLQVDLTRFGNLKNGVNDIKNHWFAATDWTIAIYQRKVEAPPFKFG 320

RESULT 12

SCH9_YEAST

ID SCH9_YEAST STANDARD; PRT; 823 AA.

AC P11792;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Serine/threonine-protein kinase SCH9 (EC 2.7.1.37).

GN SCH9 OR KOM1 OR YHR205W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88255839; PubMed=3290050;

RA Toda T., Cameron S., Sass P., Wigler M.;

RT "SCH9, a gene of Saccharomyces cerevisiae that encodes a protein

RT distinct from, but functionally and structurally related to, CAMP-

RT dependent protein kinase catalytic subunits.";

RL Genes Dev. 2:517-527(1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=JR26-19D;

RX MEDLINE=93182531; PubMed=8442384;

RA di Blasi F., Carra E., de Vendittis E., Masturzo P., Burderi E.,

RA Lambrinoudaki I., Mirisola M.G., Seidita G., Pasano O.;

RT "The SCH9 protein kinase mRNA contains a long 5' leader with a small

RT open reading frame.";

RL Yeast 9:21-32(1993).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RX MEDLINE=94378003; PubMed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,

RA Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,

RA Vaudin M.;

RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

RT VIII.";

RL Science 265:2077-2082(1994).

CC -!- FUNCTION: Protein kinase that is part of growth control pathway

CC which is at least partially redundant with the cAMP pathway.

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- ENZYME REGULATION: Activated by cAMP.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP

CC subfamily.

CC -!- SIMILARITY: Contains 1 C2 domain.

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or send an email to license@isb-sib.ch).
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CC EMBL; AY083469; AAM0022.1; -.
CC PIR; C32571; C32571.
CC PIR; S30504; S30504.
CC HSSP; Q63450; 1A06.
CC MGD; MGI:104557; Rps6ka3.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IDA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 2.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 2.
DR SMART; SM00219; TyrKc; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 2.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 2.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Repeat; Multigene family; Phosphorylation.
FT DOMAIN 68 327 PROTEIN KINASE 1.
FT NP_BIND 74 82 PROTEIN KINASE 2.
FT BINDING 100 100 ATP (BY SIMILARITY).
FT ACT_SITE 193 193 ATP (BY SIMILARITY).
FT NP_BIND 428 436 BY SIMILARITY.
FT BINDING 451 451 ATP (BY SIMILARITY).
FT ACT_SITE 539 539 BY SIMILARITY.
FT MOD_RES 227 227 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 365 365 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 369 369 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 386 386 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 577 577 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 737 737 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 740 AA; 83693 MW; 0CD54E5918567007 CRC64;

Query Match 23.8%; Score 501.5; DB 1; Length 740;
Best Local Similarity 35.1%; Pred. No. 5.4e-27;
Matches 110; Conservative 66; Mismatches 118; Indels 19; Gaps 7;

Qy 11 VFDENEDVNFDFEILRAIGKGSFGEVCIVQK---NDTKKWCAKMYMNKQKCVNERNEVRN 67
Db 56 VKEGHEKADPSQFELLKVLGQSGFGKVLVKKISGSDARQLYAMKVLKATLKVRDRVRT 115

Qy 68 VFKEIQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKEBTVKLFI 127
Db 116 KM-ERDILVEVNHPPFVKLHYAFQTEGKLYLILDFLRGGDLFTRLSEKVMFTEEDVKFYL 174

Qy 128 CELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIA-AMLPREITQITTMAGTKPY 186
Db 175 AELALALDHLHSLGIYRDLKPENILLDEEGHIKLTDFGLSKESIDHEKKAYSFCTVEY 234

Qy 187 MAPEMFSSRRKGAGYSFAVDWWSLGVATAYELLRGRPPHYHRSSTSSKEIVHTFTTVTYP 246
Db 235 MAPEVNNRR---GHTQSADWWSFGVLMFEMLTGTLFP---QGKDRKETMTMILKAKLGMP 288

Qy 247 SAWSQEMVSLKKLLEBNPDQRFQSQ----LSDVQNFYPMNDINWDVAFQKRLIPGFIPNK 302
Db 289 QFLSPEAQSLRLMLFKRNPANRLGAGPDGVVEIKRHSFFSTIDWNKLYRREIHPPEKPAT 348

Qy 303 GR----LNCDPTE 311
Db 349 GRPEDTFYFDPEF 361

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RESULT 15.
YPK2_YEAST
ID   YPK2_YEAST      STANDARD;          PRT;          677 AA.
AC   P18961;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Serine/threonine-protein kinase YPK2/YKR2 (EC 2.7.1.-).
GN   YPK2 OR YKR2 OR YMR104C OR YM9718.03C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89306654; PubMed=2663649;
RA   Kubo K., Ohno S., Matsumoto S., Yahara I., Suzuki K.;
RT   "A novel yeast gene coding for a putative protein kinase.";
RL   Gene 76:177-180(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93173125; PubMed=8437590;
RA   Chen P.C., Lee K.S., Levin D.E.;
RT   "A pair of putative protein kinase genes (YPK1 and YPK2) is required
RT   for cell growth in Saccharomyces cerevisiae.";
RL   Mol. Gen. Genet. 236:443-447(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   STRAIN=S288C / AB972;
RX   MEDLINE=97313268; PubMed=9169872;
RA   Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA   Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA   Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA   Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT   XIII.";
RL   Nature 387:90-93(1997).
CC   -1- FUNCTION: Plays an essential role in the proliferation of yeast
CC   cells.
CC   -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   RAC SUBFAMILY. STRONGEST TO YPK1.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M24929; AAA78259.1; -.
DR   EMBL; Z49702; CAA89740.1; -.
DR   PIR; J50178; JS0178.
DR   HSSP; P05132; 1CTP.
DR   GerMOnline; 142772; -.
DR   SGD; S0004710; YPK2.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   InterPro; IPR000961; pkinase C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKC; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   TRANSFERase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN 35 57 HIS-RICH.
FT   DOMAIN 344 599 PROTEIN_KINASE.

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Search completed: June 25, 2004, 10:49:36
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:46:29 ; Search time 21 Seconds
(without alignments)
1813.897 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFDEDEDVNF.....NLAEQTKPQGEDQNNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	843.5	40.1	379	2 T23688	hypothetical prote
2	537	25.5	479	2 A38578	protein kinase 2 (
3	528.5	25.1	648	1 JQ1150	protein kinase (EC
4	521	24.8	480	2 S56639	ribosomal protein
5	516.5	24.5	465	2 S68462	protein kinase ATP
6	513	24.4	680	2 S37955	protein kinase YPK
7	511.5	24.3	696	2 S55694	protein kinase (EC
8	510.5	24.3	353	2 C31751	protein kinase (EC
9	508	24.1	471	2 S68463	protein kinase ATP
10	507	24.1	352	2 S19027	protein kinase A (
11	506.5	24.1	785	2 T20232	hypothetical prote
12	506	24.0	359	2 T21211	hypothetical prote
13	503	23.9	375	2 T21212	hypothetical prote
14	502.5	23.9	351	1 OKHYCA	protein kinase (EC
15	502.5	23.9	823	2 S48986	probable protein k
16	501.5	23.8	360	1 OKHUCG	protein kinase (EC
17	501.5	23.8	740	2 I38556	ribosomal protein
18	501	23.8	677	2 JS0178	protein kinase YKR
19	500.5	23.8	733	2 A57459	ribosomal protein
20	499	23.7	359	1 OKKWC1	protein kinase (EC
21	498.5	23.7	351	1 OKHU2C	protein kinase (EC
22	498.5	23.7	351	1 OKRT2C	protein kinase (EC
23	496.5	23.6	351	1 OKBO2C	protein kinase (EC
24	496	23.6	351	1 OKRTCB	protein kinase (EC
25	496	23.6	351	1 OKMSCB	protein kinase (EC
26	496	23.6	351	1 OKHYCB	protein kinase (EC
27	496	23.6	352	2 S19028	protein kinase (EC
28	496	23.6	375	1 OKKWC2	protein kinase (EC
29	495.5	23.6	586	2 A53758	protein kinase C (

30	495.5	23.6	587	2 A49509	protein kinase C (
31	495.5	23.6	689	1 A53791	beta-adrenergic-re
32	494.5	23.5	752	1 A32571	ribosomal protein
33	493.5	23.5	352	2 JC7968	cyclic adenosine 3
34	493.5	23.5	398	1 OKBYC3	protein kinase (EC
35	493.5	23.5	646	2 T38171	probable serine/th
36	493.5	23.5	689	1 A40088	beta-adrenergic-re
37	492.5	23.4	351	1 OKMSCA	protein kinase (EC
38	492.5	23.4	689	1 I56531	beta-adrenergic-re
39	492.5	23.4	1102	2 T28666	protein kinase C-r
40	491.5	23.4	733	1 B30001	ribosomal protein
41	490	23.3	334	2 A60543	protein kinase (EC
42	490	23.3	512	2 A54400	protein kinase (EC
43	488.5	23.2	629	2 A30001	ribosomal protein
44	487	23.1	380	1 OKBYC2	protein kinase (EC
45	486.5	23.1	351	1 OKHUCB	protein kinase (EC

ALIGNMENTS

RESULT 1

T23688
hypothetical protein M03C11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T23688
R;McMurray, A.
submitted to the EMBL Data Library, April 1995
A;Reference number: Z19783
A;Accession: T23688
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-379 <WIL>
A;Cross-references: EMBL:Z49128; PIDN:CAA88953.1; GSPDB:GN00021; CESP:M03C11.1
A;Experimental source: clone M03C11
C;Genetics:
A;Gene: CESP:M03C11.1
A;Map position: 3
A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match	40.1%	Score	843.5;	DB	2;	Length	379;
Best Local Similarity	44.1%	Pred. No.	5.7e-31;				
Matches	158;	Conservative	70;	Mismatches	117;	Indels	13;
Gaps	4;						
QY	22	HFEILRAIGKGSFGEVCIVQKNDTKMKCAMKYMKNQKCVNERVNVFKELQIMQGLEHP	81				
Db	27	HFSVIRSIGRGAFGKVCIVQERKTKKYFALKYMKMKRCIEKGVANVIRELTLLSKMSHP	86				
QY	82	FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNNVHFKEETVKLFICELVMALDYLNQR	141				
Db	87	FIVNLWYTFQGDYMYMVSDDLGGDLRYHLSSQGGKFAEDRAKLYLCEICLAVEYLHEMK	146				
QY	142	IIHRDMKPDNILLDEGHVHITDFTNIAAMLPRETQITTMAGTKPYMAPEMPSS--RKGAG	199				
Db	147	IVHRDIKENILLDEQGHVHITDFTNIAAMLPRETQITTMAGTKPYMAPEMPSS--RKGAG	206				
QY	200	YSPAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFTTFTVTPSAMSQEMVSLKK	259				
Db	207	YDSRVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFTTFTVTPSAMSQEMVSLKK	266				
QY	260	LLEPNPDQPSQLSDVQNFPPYNDINWDVAFQKRLIPGFI PNKGRINCDPTPELEEMILE	319				
Db	267	MLKFDKGRVLGVAIKGHSYTERIDPKSVFEKKPSPVFIPCKEGLNCDPMYEEERILV	326				
QY	320	SKPLHKKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFIIFNREKVNDRDNKRQPN	377				
Db	327	STPIH--RRRTNHNSSGRSSSEPNQALVE---VSKAFIDFSRNV-----KIEPN	373				

RESULT 2

A38578

protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)

C;Species: Dictyostelium discoideum

C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Sep-1999

C;Accession: A38578

R;Haribabu, B.; Dottin, R.P.

Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991

A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum

A;Reference number: A38578; MUID:91142122; PMID:1996312

A;Accession: A38578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <HAR>

A;Cross-references: GB:M59744; NID:g167717; PIDN:AAA33186.1; PID:g167718

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin

F;151-407/Domain: protein kinase homology <KIN>

F;159-167/Region: protein kinase ATP-binding motif

Query Match 25.5%; Score 537; DB 2; Length 479;

Best Local Similarity 36.2%; Pred. No. 2.4e-17;

Matches 117; Conservative 66; Mismatches 124; Indels 16; Gaps 6;

QY 11 VFDEN-EDVNFDFEILRAIGKSGFGEVCIVQKNDTKKMCAMKYNKQKCVNERNVNF 69

DB 140 IFSKNQSATKDDFELLNVIGKSGFGVMQVKKGEDKIFAMKVLKDAIARKQVNHK 199

QY 70 KELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFEETVKLFCE 129

DB 200 SEKTILQCTSHPPFIVNLHYAFQTKDKLYMVLDFVNGGELFFHLKRGREFSEPRVKIAAE 259

QY 130 LVMAALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAP 189

DB 260 IVSALDHLHKQDIVYRDLKPNILLSEGHICITDFGLSKKLTETDGTFTFCGTPEYLAP 319

QY 190 EMPSSRKAGYSFADVWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFETVTVVTSAP 249

DB 320 EVLN---GHGHCADVWWSLGTLLVEMLTGLPPFYSQNVSTMYQKILNGELKIPTY---I 373

QY 250 SQEMVSLKKLLEPNPDQRFSQL--SDVQNPPYMNNDINWDAVQKRLIPGPIP-----NKG 303

DB 374 SPEAKSLLEGLLTREVDRKLGTKGGGEVQKHPWFKNIDWEKLDKKEVEVHFVKPKVKSQTD 433

QY 304 RLNCDDPTFELE---EMILESXP 323

DB 434 ISQIDPVFTQRPMDSLVETSAL 456

RESULT 3

JQ1150

protein kinase (EC 2.7.1.37) CAMP-dependent, catalytic chain - slime mold (Dictyostelium

C;Species: Dictyostelium discoideum

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998

C;Accession: JQ1150

R;Buerki, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.

Gene 102, 57-65, 1991

A;Title: Isolation of two genes encoding putative protein kinases regulated during Dicty

A;Reference number: JQ1150; MUID:91323730; PMID:1864510

A;Accession: JQ1150

A;Molecule type: DNA

A;Residues: 1-648 <BUE>

A;Cross-references: GB:M38703

C;Genetics:

A;Gene: PK2

A;Introns: 578/3

C;Complex: heterodimer with regulatory chain; active catalytic chain is released when ca

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A;Note: important for cell type differentiation and fruiting body morphogenesis

C;Superfamily: Dictyostelium CAMP-dependent protein kinase catalytic chain; protein kin

C;Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specifi

F;126-223/Region: glutamine-rich

F;297-312/Region: glutamine-rich

F;334-590/Domain: protein kinase homology <KIN>

F;342-350/Region: protein kinase ATP-binding motif

F;365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted

F;464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.1%; Score 528.5; DB 1; Length 648;

Best Local Similarity 34.2%; Pred. No. 7.5e-17;

Matches 110; Conservative 76; Mismatches 115; Indels 21; Gaps 8;

QY 9 PPVFDENEVDNFDHFEILRAIGKSGFGEVCIVQKNDTKKMC--AMKYNKQKCVNERNEVR 66

DB 325 PPV---NARERLKEFKQIRVLGTGTGKVVLIQ--NTKDCGYAMKCLNKAYVVQLKQVE 379

QY 67 NVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFEETVKLF 126

DB 380 HLNSEKSLSSIHPPFIVNLVYQAFQDEKLLYLLFEYVAGGEVFTHLRKSMEFSTAKFY 439

QY 127 ICELVMAALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPY 186

DB 440 AAEIVLALEFLHKQNIYRDLKPNILLIDNQGHKIKITDFGFAKRV--EDRTFILCGTPEY 497

QY 187 MAPEMFSSRKAGYSFADVWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFETVTVVTP 246

DB 498 LAPEIIQSK---GHGKAVDWWALGILIFELMAGYPPFY---DDDTFAIYNKILAGRITFP 551

QY 247 SAMSQEMVSLKKLLEPNPDQRFSQLS---DVQNPPYMNNDINWDAVQKRLIPGFI PNK 302

DB 552 LGFDVDAKOLIKRLLTADRTTRRLGALKDQALDVKNHRWFS DINWERYQRDNGPFIPIKI 611

QY 303 GRNLCDPTFEL--EEMILESXP 322

DB 612 QHQGDSSNFEMYDEEMVEEPP 633

RESULT 4

S56639

ribosomal protein S6 kinase homolog (clone Aspk11) - oat

N;Alternate names: mitogen-activated protein kinase pp70 homolog

C;Species: Avena sativa (oat)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C;Accession: S56639

R;Huttly, A.K.; Phillips, A.L.

Plant Mol. Biol. 27, 1043-1052, 1995

A;Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that s

A;Reference number: S56638; MUID:95284341; PMID:7766874

A;Accession: S56639

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-480 <HUT>

A;Cross-references: EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g871986

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; phosphotransferase; protein kinase

F;149-407/Domain: protein kinase homology <KIN>

F;157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 521; DB 2; Length 480;

Best Local Similarity 35.3%; Pred. No. 1.2e-16;

Matches 107; Conservative 62; Mismatches 124; Indels 10; Gaps 3;

QY 14 ENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKMCAMKYNKQKCVNERNVNFKELQ 73

DB 142 ENEAVGLDNFEVLKLVGGAGFGKVVQVRMKGTSIYAMKVMRKDKILEKTHAEYMKAEKD 201

QY 74 IMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNVHFEETVKLFCELVMA 133

DB 202 ILTKVDHPFVQVQLRYSFQTKYRLYLVLDFVNGGHLFFQLYQQGLFREELARIYTAELVSA 261

QY 134 LDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMS 193

DB 262 VAHLHANGIMHRDLKPNILLDARGHAMLTDFGLAKEFDENTRSNMGCTVEYMAPEIV- 320

QY 194 SRKAGYSFADVWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFETVTVVTPSAWSQEM 253

DB 321 --QGRGHDKAADWWSVIGILLFEMLTGKPPFF---GGRDKIQKIVREKMKLPSYLSSEV 375

A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 24.0%; Score 506; DB 2; Length 359;
Best Local Similarity 33.0%; Pred. No. 4.5e-16;
Matches 109; Conservative 78; Mismatches 121; Indels 22; Gaps 7;

QY 14 ENEDVN---FDHFEILRAIGKSGFGEVCIVQKNDTKQKCMKYMKNKQKCVNERNEVRNVFK 70
Db 40 ENPAQNTACLDDEFDRIKTLGTGSGFGRVMLVKHKQSGNYAMKILDQKVVKLQKVEHTLN 99
QY 71 ELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKETVKLFICEL 130
Db 100 EKRILOAIDFPFLVNMWTFKONSNLVWLEFISGGMFSLRRIGRPFSEPHSRFYAAQI 159
QY 131 VMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPE 190
Db 160 VLAPEYLHSLDIYRDLKPENLLIDSTGYLKITDFGAKRVKGR--WTLCGTPEYLAPE 217
QY 191 MFSSRKGAGYSFAVDWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTFETTV---VTYPS 247
Db 218 IILSK---GYNKAVDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVFPFS 268
QY 248 AWSQEMVSLKLLPENPDQRFSQL-----SDVQNFPPYMNNDINWDAVFQKRLIPGFIPN-K 302
Db 269 HFSNELKDLLKNLLQVLDLTKRYGNLKNGVADIKNHKWFSGSTDWIAIYQKKIEAPFLPKCR 328
QY 303 GRLNCDPTFEELEEMILESPLHKKKKRLAK 332
Db 329 GPGDASNFDDYEEPLRISGTEKCAKEFAE 358

RESULT 13
T21212
hypothetical protein ZK909.2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T21212; T28101
R;McLay, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19391
A;Accession: T21212
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Cross-references: EMBL:Z81511; PIDN:CAB04169.1; GSPDB:GN00019; CESP:ZK909.2b
A;Experimental source: clone F21F12
R;White, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20469
A;Accession: T28101
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-375 <WI2>
A;Cross-references: EMBL:Z82096; PIDN:CAB05035.1; GSPDB:GN00019; CESP:ZK909.2b
A;Experimental source: clone ZK909
C;Genetics:
A;Gene: CESP:ZK909.2b
A;Map position: 1
A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.9%; Score 503; DB 2; Length 375;
Best Local Similarity 34.3%; Pred. No. 6.3e-16;
Matches 104; Conservative 74; Mismatches 103; Indels 22; Gaps 7;

QY 14 ENEDVN---FDHFEILRAIGKSGFGEVCIVQKNDTKQKCMKYMKNKQKCVNERNEVRNVFK 70
Db 40 ENPAQNTACLDDEFDRIKTLGTGSGFGRVMLVKHKQSGNYAMKILDQKVVKLQKVEHTLN 99
QY 71 ELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKETVKLFICEL 130
Db 100 EKRILOAIDFPFLVNMWTFKONSNLVWLEFISGGMFSLRRIGRPFSEPHSRFYAAQI 159

QY 131 VMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPE 190
Db 160 VLAPEYLHSLDIYRDLKPENLLIDSTGYLKITDFGAKRVKGR--WTLCGTPEYLAPE 217
QY 191 MFSSRKGAGYSFAVDWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTFETTV---VTYPS 247
Db 218 IILSK---GYNKAVDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVFPFS 268
QY 248 AWSQEMVSLKLLPENPDQRFSQL-----SDVQNFPPYMNNDINWDAVFQKRLIPGFIPNKG 303
Db 269 HFSNELKDLLKNLLQVLDLTKRYGNLKNGVADIKNHKWFSGSTDWIAIYQKKITPPSF-SKG 327
QY 304 RLN 306
Db 328 ESN 330

RESULT 14
OKHYCA
protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999
C;Accession: B40384
R;Howard, P.; Day, K.H.; Kim, K.E.; Richardson, J.; Thomas, J.; Abraham, I.; Fleischm.
J. Biol. Chem. 266, 10189-10195, 1991
A;Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA s;
A;Reference number: A40384; MUID:91244783; PMID:1645343
A;Accession: B40384
A;Molecule type: mRNA
A;Residues: 1-351 <HOW>
A;Cross-references: GB:M63311; NID:G191174; PIDN:AAA37010.1; PID:G191175
C;Comment: The inactive enzyme contains two regulatory chains and two catalytic chain;
. Two types found in mammalian tissue are distinguished by having either type I or ty
C;Comment: Both alpha and beta catalytic chains are found in many tissues, with the a
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; blocked amino end; cAMP binding; heterotetramer; lipoprotein; magnes
P;2-351/Product: protein kinase, cAMP-dependent, alpha catalytic chain #status predic
P;42-298/Domain: protein kinase homology <KIN>
P;50-58/Region: protein kinase ATP-binding motif
P;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
P;3/Modified site: aspartic acid (Asn) #status predicted
P;11,339/Binding site: phosphate (Ser) (covalent) #status predicted
P;55,56,122,128,171,184/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Thr) #status p
P;73,92,167,169/Active site: Lys, Glu, Asp, Lys #status predicted
P;172,185/Binding site: magnesium (Asn, Asp) #status predicted
P;198/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 23.9%; Score 502.5; DB 1; Length 351;
Best Local Similarity 34.0%; Pred. No. 6.2e-16;
Matches 99; Conservative 76; Mismatches 97; Indels 19; Gaps 6;

QY 21 DHFEILRAIGKSGFGEVCIVQKNDTKQKCMKYMKNKQKCVNERNEVRNVFKELQIMQGLEH 80
Db 42 DHFDRIKTLGTGSGFGRVMLVKHETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVNF 101
QY 81 PFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKETVKLFICELVMALDYLNQ 140
Db 102 PFLVKLEFSFKDONSILYMWMEVPGGEMFSLRRIGRPFSEPHARFYAAQIVLTFEYLHSL 161
QY 141 RIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSSRKGAGY 200
Db 162 DLIYRDLKPENLLIDQGGYIQVTDGFAKRVKGR--WTLCGTPEYLAPEIILSK---GY 216
QY 201 SFVDWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTFETTV---VTYPSAWSQEMVSL 257
Db 217 NKAVDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVRFPFSFSSDLKDLL 270
QY 258 KKLEPNPDQRFSQL-----SDVQNFPPYMNNDINWDAVFQKRLIPGFIPN-KG 303
Db 271 RNLLQVLDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQKRVKVEAPFIPKPKG 321

Search completed: June 25, 2004, 10:50:09
Job time : 22 secs

RESULT 15

S48986
probable protein kinase SCH9 (EC 2.7.1.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR205W
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Sep-1999
C;Accession: S48986; S30022; A28429
R;Macri, C.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of S. cerevisiae cosmid 9177.
A;Reference number: S46671
A;Accession: S48986
A;Molecule type: DNA
A;Residues: 1-823 <MAC>
A;Cross-references: EMBL:U00029; NID:G551322; PIDN:AAB69735.1; PID:G458923; MIPS:YHR205W
R;di Blasi, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I.
Yeast 9, 21-32, 1993
A;Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading
A;Reference number: S30021; MUID:93182531; PMID:8442384
A;Accession: S30022
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M', 1-823 <DIB>
A;Cross-references: EMBL:X57629; NID:G5277; PIDN:CAA40853.1; PID:G5279
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991
R;Toda, T.; Cameron, S.; Sass, P.; Wigler, M.
Genes Dev. 2, 517-527, 1988
A;Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from,
A;Reference number: A28429; MUID:88255839; PMID:3290050
A;Accession: A28429
A;Molecule type: DNA
A;Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>
A;Cross-references: EMBL:X12560; NID:G4425; PIDN:CAA31073.1; PID:G4426
C;Genetics:
A;Gene: SGD:SCH9
A;Cross-references: SGD:S0001248; MIPS:YHR205W
A;Map position: 8R
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;409-670/Domain: protein kinase homology <KIN>
F;417-425/Region: protein kinase ATP-binding motif

Query Match		23.9%	Score 502.5;	DB 2;	Length 823;
Best Local Similarity		35.3%	Pred. No. 1.3e-15;		
Matches		118;	Conservative 68;	Mismatches 113;	Indels 35; Gaps 10;
QY	6	SRKPPVFDE--NEDVNF-----	DHFEILRAIGKSGFGEVCIVQKNDTKMC	49	
Db	378	SLKPRVIDEVVSGDILIKTYKTKRHYGPQDFEVLRLGKTFGQYQVKKKDTQRIY	437		
QY	50	AMKYNNKQKCVERNEVRNVFKEIQIM---	QGLEHPFLVNLWYSPQDEEDMFVVVDLLGG	106	
Db	438	AMKVLKKKVIIVKKEIAHTIGERNILVTTASKSSPFIVGLKPSFQPTDLYLVTDYMSGG	497		
QY	107	DLRYHLQONVHFKEETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFN	166		
Db	498	ELFWHLQKEGRFSEDRAKFYIAELVLALEHLHDNDIVYRDLKPENILLDANGNIALCDFG	557		
QY	167	IA-AMLPRETQITTMAGTKPYMAPEMFSSRKAGYSFVDMWSLGVATAYELLGRRPYHI	225		
Db	558	LSKADLKORT--NTFCGTTEYLAPELLLDE--	TGYTKMVDLFWSLGLVIFEMCCGWSPPFF-	612	
QY	226	RSSTSSKEIVHTFTTIVTYP-SAWSQEMVSLKKLEPNPDQRFSQLSD---	VQNFPPYM	281	
Db	613	--AENNQMYQKIAFGKVKFPRDVLSEGRSFVKGLNRPKRLGAIDDDRELRAHPFF	670		
QY	282	NDINWDVAFQKRLIPGFIPN----	KGRNCDPTF	311	
Db	671	ADIDWEALKQKIPPPFKPLVSETDTSNFDPEF	704		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:50:15 ; Search time 48 Seconds
(without alignments)
2329.088 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFEDENEDVNF.....NLAEQTKOPQGEDQNNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2104	100.0	396	9	US-09-801-876B-2
2	2104	100.0	396	12	US-10-667-442-2
3	2104	100.0	396	14	US-10-254-869-2
4	2089	99.3	396	9	US-09-841-683-11
5	2089	99.3	396	12	US-10-362-892-20
6	2089	99.3	396	12	US-10-182-243-33
7	2089	99.3	396	15	US-10-288-798-20
8	2083	99.0	396	15	US-10-410-764-101
9	2047	97.3	407	9	US-09-841-683-9
10	1814	86.2	358	15	US-10-108-260A-2674
11	1437.5	68.3	414	15	US-10-074-978A-158
12	1427	67.8	404	9	US-09-801-876B-4
13	1427	67.8	404	12	US-10-667-442-4
14	1427	67.8	404	14	US-10-254-869-4
15	1425.5	67.8	403	9	US-09-801-876B-5

16	1425.5	67.8	403	12	US-10-667-442-5	Sequence 5, Appli
17	1425.5	67.8	403	14	US-10-254-869-5	Sequence 5, Appli
18	1425.5	67.8	414	14	US-10-354-358-36	Sequence 36, Appl
19	1425.5	67.8	414	15	US-10-074-978A-157	Sequence 157, App
20	1324	62.9	419	9	US-09-799-875-14	Sequence 14, Appl
21	1324	62.9	419	12	US-10-649-156-14	Sequence 14, Appl
22	1324	62.9	419	14	US-10-303-664A-6	Sequence 6, Appli
23	1318	62.6	485	12	US-10-415-011-12	Sequence 12, Appl
24	1317.5	62.6	384	9	US-09-801-876B-6	Sequence 6, Appli
25	1317.5	62.6	384	12	US-10-667-442-6	Sequence 6, Appli
26	1317.5	62.6	384	14	US-10-254-869-6	Sequence 6, Appli
27	1317.5	62.6	488	15	US-10-074-978A-154	Sequence 154, App
28	1302	61.9	488	15	US-10-074-978A-18	Sequence 18, Appl
29	1278.5	60.8	399	10	US-09-819-607-4	Sequence 4, Appli
30	1278.5	60.8	399	12	US-10-633-631-4	Sequence 4, Appli
31	1259.5	59.9	375	12	US-10-168-582-12	Sequence 12, Appl
32	1201.5	57.1	364	12	US-10-206-915-572	Sequence 572, App
33	1201.5	57.1	364	12	US-10-199-670-572	Sequence 572, App
34	1201.5	57.1	364	12	US-10-201-858-572	Sequence 572, App
35	1201.5	57.1	364	12	US-10-205-890-572	Sequence 572, App
36	1201.5	57.1	364	12	US-10-208-024-572	Sequence 572, App
37	1201.5	57.1	364	12	US-10-201-853-572	Sequence 572, App
38	1201.5	57.1	364	12	US-10-174-581-572	Sequence 572, App
39	1201.5	57.1	364	12	US-10-176-483-572	Sequence 572, App
40	1201.5	57.1	364	12	US-10-176-749-572	Sequence 572, App
41	1201.5	57.1	364	12	US-10-176-914-572	Sequence 572, App
42	1201.5	57.1	364	12	US-10-176-915-572	Sequence 572, App
43	1201.5	57.1	364	12	US-10-176-484-572	Sequence 572, App
44	1201.5	57.1	364	12	US-10-180-550-572	Sequence 572, App
45	1201.5	57.1	364	12	US-10-183-014-572	Sequence 572, App

ALIGNMENTS

RESULT 1

US-09-801-876B-2
; Sequence 2, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-2

Query Match	100.0%	Score 2104;	DB 9;	Length 396;
Best Local Similarity	100.0%	Pred. No. 5e-169;		
Matches 396;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGANTSRKPPVFEDENEDVNF	1	MGANTSRKPPVFEDENEDVNF
Db	1	MGANTSRKPPVFEDENEDVNF	1	MGANTSRKPPVFEDENEDVNF
QY	61	ERNEVRNVFKELQIMQGLEHP	61	ERNEVRNVFKELQIMQGLEHP
Db	61	ERNEVRNVFKELQIMQGLEHP	61	ERNEVRNVFKELQIMQGLEHP
QY	121	ETVKLFICELVMALDYLNQRI	121	ETVKLFICELVMALDYLNQRI
Db	121	ETVKLFICELVMALDYLNQRI	121	ETVKLFICELVMALDYLNQRI
QY	181	AGTKPYMAPEMFSSRKAGYS	181	AGTKPYMAPEMFSSRKAGYS
Db	181	AGTKPYMAPEMFSSRKAGYS	181	AGTKPYMAPEMFSSRKAGYS

Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396

RESULT 2
US-10-667-442-2
; Sequence 2, Application US/10667442
; Publication No. US20040043466A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-667-442-2

Query Match 100.0%; Score 2104; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-169;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396

RESULT 3
US-10-254-869-2
; Sequence 2, Application US/10254869
; Publication No. US20030027307A1
; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match 100.0%; Score 2104; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-169;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKKLLPNPDQRFSDVQNFYPMNDINWDVAVFQKRLIPGFI 300
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPQNLALAEQTKDPQGEDGQNNNL 396

RESULT 4
US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotide
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens

US-09-841-683-11

Query Match 99.3%; Score 2089; DB 9; Length 396;
Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MGANTSRKPPVDFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKMCAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHIRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 5

US-10-362-892-20
; Sequence 20, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Damiel B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389

; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CD1
US-10-362-892-20

Query Match 99.3%; Score 2089; DB 12; Length 396;
Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGANTSRKPPVDFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKMCAMKYNKQKCV 60
Db 1 MGANTSRKPPVDFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKMCAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHIRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 6

US-10-182-243-33
; Sequence 33, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-243-33

Query Match 99.3%; Score 2089; DB 12; Length 396;


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; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-764-101

Query Match          99.0%; Score 2083; DB 15; Length 396;
Best Local Similarity 99.2%; Pred. No. 3e-167;
Matches 393; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240

Qy 241 TVTYPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFI 300
Db 241 TVTYPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFI 300

Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNDRFNKRPNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRFNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 9
US-09-841-683-9
; Sequence 9, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-9

Query Match          97.3%; Score 2047; DB 9; Length 407;
Best Local Similarity 98.7%; Pred. No. 3.3e-164;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHTFET 240

Qy 241 TVTYPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFI 300
Db 241 TVTYPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNFYPMNDINWDVAFQKRLIPGFI 300

Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNDRFNKRPNLALAEQTKDPQGEDGQ 392
Db 361 IFNREKVNDRFNKRPNLALAEQTKDPQVTNGQ 392

RESULT 10
US-10-108-260A-2674
; Sequence 2674, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2674
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2674

Query Match          86.2%; Score 1814; DB 15; Length 358;
Best Local Similarity 99.4%; Pred. No. 1.3e-144;
Matches 342; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKMKCAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180
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QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLGRPPYHRSSTSSKEIVHTFET 240
QY 241 TVVTPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300
Db 241 TVVTPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKCDSSQ 344
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKCDSSQ 344

RESULT 11

US-10-074-978A-158
; Sequence 158, Application US/10074978A
; Publication No. US20040010119A1

GENERAL INFORMATION:

; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-074-978A-158

Query Match 68.3%; Score 1437.5; DB 15; Length 414;
Best Local Similarity 69.7%; Pred. No. 8.6e-113;
Matches 278; Conservative 38; Mismatches 64; Indels 19; Gaps 3;
QY 1 MGANTSRKPPVFDENEDVDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Db 1 MGNHSHKPPVFDENEVDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120
QY 121 ETVKLFICELVMDLYLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIPDNILLDEHGHVHITDFNIAVLKSGEKASSM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVATAYELLGRPPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVQVYVDGGPGYSYPVDWWSLGVATAYELLGRPPYHRSSTSSKEIVHTF 240
QY 239 ETTVTPSAWSQEMVSLKLLLEPNPDQRFSQLSDVQNPFPYMDINWDVAFQKRLIPGF 298
Db 241 KVERVHYSSTWCEGMVSLKLLTKDPESSRLSLRDIQSMYTLADMNDWDAVPEKALMPGF 300
QY 299 IPNKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKCDSSQTCLLQEHLDVQK 357
Db 301 VPNGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKCDSSQTCLLQEHLDVQK 360
QY 358 EPIIFNREKVNDRFNKQPNLALEQTKDPQGEDCQNNNL 396
Db 361 EPIIFNREKLRQ-----QGHGQLSDL 383

RESULT 12

US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-4

Query Match 67.8%; Score 1427; DB 9; Length 404;
Best Local Similarity 69.5%; Pred. No. 6.4e-112;
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;
QY 1 MGANTSRKPPVFDENEDVDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
Db 1 MGNHSHKPPVFDENEVDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60
QY 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119

Db 61 QERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVLKSEKASS 180
QY 180 MAGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVATAYELLRGRWPYEHISATPIDEILNM 240
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPG 297
Db 241 FKVERVHYSSTWCEGMVSLKLLTKDPESRLSSLDIQSMTYLDNMWDVAFKALMPG 300
QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356
Db 301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAKHRSRDSKSCPLNGHLQOCLETVR 360
QY 357 KEFIIFNREKVNDRFNKRPQNLALAEQTKDPQGEDGQNNNL 396
Db 361 KEFIIFNREKLRQ-----QGHGQLSDL 384

RESULT 13
US-10-667-442-4
; Sequence 4, Application US/10667442
; Publication No. US20040043466A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-667-442-4

Query Match 67.8%; Score 1427; DB 12; Length 404;
Best Local Similarity 69.5%; Pred. No. 6.4e-112;
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;
QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKGMCKMYMKQKCV 60
Db 1 MGGNHSKPPVFDENEVNFDFHFEILRAIGKSGFGEVCIVQKNDTKGMCKMYMKQKCV 60
QY 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 119
Db 61 QERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVLKSEKASS 180
QY 180 MAGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVATAYELLRGRWPYEHISATPIDEILNM 240
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPG 297
Db 241 FKVERVHYSSTWCEGMVSLKLLTKDPESRLSSLDIQSMTYLDNMWDVAFKALMPG 300
QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356
Db 301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAKHRSRDSKSCPLNGHLQOCLETVR 360
QY 357 KEFIIFNREKVNDRFNKRPQNLALAEQTKDPQGEDGQNNNL 396

Db 361 KEFIIFNREKLRQ-----QGHGQLSDL 384
RESULT 14
US-10-254-869-4
; Sequence 4, Application US/10254869
; Publication No. US20030027307A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-4

Query Match 67.8%; Score 1427; DB 14; Length 404;
Best Local Similarity 69.5%; Pred. No. 6.4e-112;
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;
QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKGMCKMYMKQKCV 60
Db 1 MGGNHSKPPVFDENEVNFDFHFEILRAIGKSGFGEVCIVQKNDTKGMCKMYMKQKCV 60
QY 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 119
Db 61 QERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVLKSEKASS 180
QY 180 MAGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVATAYELLRGRWPYEHISATPIDEILNM 240
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPG 297
Db 241 FKVERVHYSSTWCEGMVSLKLLTKDPESRLSSLDIQSMTYLDNMWDVAFKALMPG 300
QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356
Db 301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAKHRSRDSKSCPLNGHLQOCLETVR 360
QY 357 KEFIIFNREKVNDRFNKRPQNLALAEQTKDPQGEDGQNNNL 396
Db 361 KEFIIFNREKLRQ-----QGHGQLSDL 384

RESULT 15
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403

TYPE: PRT
ORGANISM: Human
US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 9; Length 403;
Best Local Similarity 68.2%; Pred. No. 8.5e-112;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY	1	MGANTSRKPPVPDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMCMYNNKQCV	60
Db	1	MGGNHSHKPPVPDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMCMYNNKQCV	60
QY	61	ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK	120
Db	61	ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK	120
QY	121	ETVKLPICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180
Db	121	GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVVKGAERASSM	180
QY	181	AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPYHIRSSTSSKEIVHTF	238
Db	181	AGTKPYMAPEVFQVYMDRGPYSYPVDWWSLGVATAYELLRGRPPYHISVTPIDEILNMF	240
QY	239	ETTVVTYPSAWSQEMVSLKLLLEPNPDQFSLQSDVQNPFPYMDINWDVAFQKRLIPGF	298
Db	241	KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLDIQSVPYLADMNWDVAFKKALMPGF	300
QY	299	IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK	357
Db	301	VPNKGRLNCDPTFELEEMILESPLHKKKRLAKNRSRDGTCDSCPLNGHLQHCLETVRE	360
QY	358	EFILFNREKVNRFNKRQPNLALQTKDPQ-----EDGQNNNL	396
Db	361	EFILFNREKLRQQGGSQQLDSDSRGGGQAQSKLDGCGNNNL	403

Search completed: June 25, 2004, 10:56:33
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:48:00 ; Search time 23 Seconds
(without alignments)
888.865 Million cell updates/sec

Title: US-10-667-442-2
Perfect score: 2104
Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLALQTKDPQGEDGQNNL 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	396	4	US-09-801-876B-2
2	2104	100.0	396	4	US-10-254-869-2
3	2089	99.3	396	4	US-09-841-683-11
4	2047	97.3	407	4	US-09-841-683-9
5	1427	67.8	404	4	US-09-801-876B-4
6	1427	67.8	404	4	US-10-254-869-4
7	1425.5	67.8	403	4	US-09-801-876B-5
8	1425.5	67.8	403	4	US-10-254-869-5
9	1324	62.9	419	4	US-09-799-875-14
10	1317.5	62.6	384	4	US-09-801-876B-6
11	1317.5	62.6	384	4	US-10-254-869-6
12	1278.5	60.8	399	4	US-09-819-607-4
13	1161	55.2	236	4	US-09-841-683-7
14	1158	55.0	225	4	US-09-841-683-5
15	1137.5	54.1	369	4	US-09-819-607-2
16	1122.5	53.4	368	4	US-09-819-607-5
17	1010.5	48.0	316	4	US-09-801-876B-7
18	1010.5	48.0	316	4	US-10-254-869-7
19	843.5	40.1	347	4	US-09-801-876B-8
20	843.5	40.1	347	4	US-10-254-869-8
21	498.5	23.7	336	4	US-09-394-455-2
22	498.5	23.7	343	4	US-09-394-455-15
23	498.5	23.7	343	4	US-09-394-455-34
24	498.5	23.7	351	4	US-09-394-455-4
25	495.5	23.6	587	1	US-08-313-274-2
26	493.5	23.5	689	1	US-08-221-817-18
27	493.5	23.5	689	1	US-08-454-439-18

28	493.5	23.5	689	5	PCT-US94-10487-18	Sequence 18, Appl
29	492.5	23.4	343	4	US-09-394-455-38	Sequence 38, Appl
30	492.5	23.4	350	4	US-09-457-040B-37	Sequence 37, Appl
31	492.5	23.4	351	4	US-09-457-040B-6	Sequence 6, Appl
32	492.5	23.4	595	4	US-09-417-197-69	Sequence 69, Appl
33	480.5	22.8	699	1	US-08-221-817-20	Sequence 20, Appl
34	480.5	22.8	699	1	US-08-454-439-20	Sequence 20, Appl
35	480.5	22.8	699	5	PCT-US94-10487-20	Sequence 20, Appl
36	474	22.5	260	2	US-07-857-224B-8	Sequence 8, Appl
37	473	22.5	260	2	US-07-857-224B-7	Sequence 7, Appl
38	469.5	22.3	688	1	US-08-221-817-19	Sequence 19, Appl
39	469.5	22.3	688	1	US-08-454-439-19	Sequence 19, Appl
40	469.5	22.3	688	5	PCT-US94-10487-19	Sequence 2, Appl
41	469	22.3	500	1	US-07-980-526-2	Sequence 15, Appl
42	469	22.3	500	1	US-08-221-817-15	Sequence 15, Appl
43	469	22.3	500	1	US-08-454-439-15	Sequence 4, Appl
44	469	22.3	500	4	US-09-614-748A-4	Sequence 15, Appl
45	469	22.3	500	5	PCT-US94-10487-15	

ALIGNMENTS

RESULT 1
US-09-801-876B-2
; Sequence 2, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
; US-09-801-876B-2

Query Match	100.0%;	Score 2104;	DB 4;	Length 396;
Best Local Similarity	100.0%;	Pred. No. 1.6e-194;		
Matches 396;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV	60	
Db	1	MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV	60	
QY	61	ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKE	120	
Db	61	ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKE	120	
QY	121	ETVKLFICELVMDLYLQNRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180	
Db	121	ETVKLFICELVMDLYLQNRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180	
QY	181	AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLRRRPHYHRSSTSSKEIVHTFET	240	
Db	181	AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVYAYELLRRRPHYHRSSTSSKEIVHTFET	240	
QY	241	TVVTPSAWSQEMVSIKKLLEPNPDQRFSDVQNFPPYMNNDINWDVAFQKRLIPGFIP	300	
Db	241	TVVTPSAWSQEMVSIKKLLEPNPDQRFSDVQNFPPYMNNDINWDVAFQKRLIPGFIP	300	
QY	301	NGRLNCDPTEFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVSQKEFI	360	
Db	301	NGRLNCDPTEFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVSQKEFI	360	
QY	361	IFNRKVNDRDNKQPNLALQTKDPQGEDGQNNNL	396	

Db 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 2

US-10-254-869-2
; Sequence 2, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match 100.0%; Score 2104; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.6e-194;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMAMKMKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMAMKMKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMPSSRRKGAGYSFVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMPSSRRKGAGYSFVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKKLLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db 241 TVVTYPSAWSQEMVSLKKLLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKCKMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKCKMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 3

US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11

Query Match 99.3%; Score 2089; DB 4; Length 396;
Best Local Similarity 99.5%; Pred. No. 4.4e-193;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMAMKMKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMAMKMKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMPSSRRKGAGYSFVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMPSSRRKGAGYSFVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKKLLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db 241 TVVTYPSAWSQEMVSLKKLLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKCKMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKKRLAKKCKMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396
Db 361 IFNREKVNDRDNKRPNLALAEQTKDPQGEDGQNNNL 396

RESULT 4

US-09-841-683-9
; Sequence 9, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-9

Query Match 97.3%; Score 2047; DB 4; Length 407;
Best Local Similarity 98.7%; Pred. No. 5.1e-189;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db	1	MGANTSRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKCMAMKYMNKQKCV	60
QY	61	ERNEVRNVFKELIQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKE	120
Db	61	ERNEVRNVFKELIQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKE	120
QY	121	ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180
Db	121	ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180
QY	181	AGTKPYMAPEMFSSRKAGYSFVDMWSLGVATAYELLRGRRPYHIRSTSSKEIVHTFET	240
Db	181	AGTKPYMAPEMFSSRKAGYSFVDMWSLGVATAYELLRGRRPYHIRSTSSKEIVHTFET	240
QY	241	TVVTYPSAWSQEMVSLKKLLEPNPDRFSQSDVQNFPPYMNNDINWDVQKRLIPGFIP	300
Db	241	TVVTYPSAWSQEMVSLKKLLEPNPDRFSQSDVQNFPPYMNNDINWDVQKRLIPGFIP	300
QY	301	NKGRNLNCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI	360
Db	301	NKGRNLNCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI	360
QY	361	IFNREKVNDRDNKRQPNLALEQTDPQEDGQ	392
Db	361	IFNREKVNDRDNKRQPNLALEQTDPQVNTGQ	392

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RESULT 5
US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-09-801-876B-4

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	Query Match	67.8%;	Score 1427;	DB 4;	Length 404;
	Best Local Similarity	69.5%;	Pred. No. 3e-129;		
	Matches 278; Conservative	38;	Mismatches 64;	Indels 20;	Gaps 4;
Qy	1	MGANTSRKPPVFDE	NEDVNFDFHFEILRAIGKSGFGEVCIVQKNPTKMKCAMKYMNKKQKV	60	
Dd	1	MGGNHSHKPPVFDE	NEEVNFDHFQILLRAIGKSGFKVCIVQKRDTCKMYAMKYMNKKQKV	60	
Qy	61	-ERNEVRNVFKELQIMOGLEHPFLVNLWYSFODEEDMFMVVDLLGGDLRYHLQQNVHFK	119		
Dd	61	QERDEVNRNVRELQIMOGLEHPFLVNLWYSPQDEEDMFMVVDLLGGDLRYHLQQNVHFT	120		
Qy	120	EETVKLPICELVMALDYLQNQRRIHRDMKPDNILLDEGHGVHITDENIAAMLPRETOITT	179		
Dd	121	EGTVKLYICELALALEYLQRYHIHRDIKPDNILLDEGHGVHITDENIATVLKGSEKASS	180		
Qy	180	MAGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLGRRRPYPHYRSSTSSKEIVHT	237		
Dd	181	MAGTKPYMAPEVFQVYVDGPGYSYPVDWWSLGVTAYELLRGMWRPYEIHSA TPIDEILNM	240		
Qy	238	FETT VVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDVA VFQXRLIP	297		
Dd	241	FKVERHY SSTWC EGMVSL LKCLLT KD PFSRLS SLRD IQSMTYLAD MNWDVA VF EKALMPG	300		

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QY 298 FIPNKGRLNCDDPTFEEEMILESKPLHKGGKRLAK-KEKMRKCDSSQTCLQEHLDVQ 356
Db 301 FVPNKGRLNCDDPTFEEEMILESKPLHKGGKRLAKHRSRDKSCPLNGHLQCCLETVR 360
QY 357 KEFIIIFNREKVNDRDNKRQPNLALBQTKDPQGEDGQNNNL 396
Db 361 KEFIIIFNREKLRQ-----QGHDGQLSDL 384

RESULT 6
US-10-254-869-4
; Sequence 4, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-4

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Query Match	67.8%;	Score 1427;	DB 4;	Length 404;
Best Local Similarity	69.5%;	Pred. No. 3e-129;		
Matches 278;	Conservative 38;	Mismatches 64;	Indels 20;	Gaps 4;

Qy	1	MGANTSRKPPVFDENEDVNFDFHFELRAIGKSGFGEVCIVQKNDTKMKCAMKMNKQKCV	60
Db	1	MGGNHSKPPVFDNEEVDNFDFHFIILRAIGKSGFGKVCIVQKRDTKKQYAMKMNKQKCV	60
Qy	61	-ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPK	119
Db	61	QERDEVNRVRELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFT	120
Qy	120	BETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEGHGVHITDENIAAMLPRETQITT	179
Db	121	EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHGVHITDENIATVLKSGEKASS	180
Qy	180	MAGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVATAYELLGRRPYPYHRSSTSSKEIVHT	237
Db	181	MAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVATAYELLGRWRPYEIHSA TPDEILNM	240
Qy	238	FETTVVTYPSAWSQEMVSLKKLLLEPNPDQRFSQLSDVQNFPPYMN DINWD AVFQKELIPG	297
Db	241	FKVERVHYSSYTCWCEGMVSLKKLLTKDPESRLSSLRDIQSMTYLADMNDWDAVFEKALMPG	300
Qy	298	FIPNKGRLNCDPTFELEEMILES KPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVSQ	356
Db	301	FVPNKGRLNCDPTFELEEMILES KPLHKKKKRLAKHRSRSDSTKDCPLNGHLQOCLJTVR	360
Qy	357	KEFIIIFNREKVRNDFNKRQPNLAL EQTKOPQGEDGQNNNL	396
Db	361	KEFIIIFNREKLRRQ-----QGHDGQLSDL	384

RESULT 7
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160

; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 4; Length 403;
Best Local Similarity 68.2%; Pred. No. 4.1e-129;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGNANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDENEENVDHFDHFIILRAIGKSGFGKVCIVQKRDTKKMYAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFAAAMLPRETOITTM 180
DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFAAATVVKGAERASSM 180
QY 181 AGTKPYMAPEMES--SRKGAGYSPAVDWSLGVATAYELLRGRPPYHRSSTSSKEIVHTE 238
DB 181 AGTKPYMAPEVQVYMDRGPYSPVDWWSLGITAYELLRGRWPYEHSTVTPIDEILNMF 240
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQRFSDVQNSDQVFPYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSYTWCKGMVALLRKLTKDPESRVSSLDHDIQSVPYLADNMWDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKMRKCDSSQTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKRLAKNRSDGTCKDSCPLNGHLQHCLETVRE 360
QY 358 EFIFNREKVRNDFNKRQPNLALAEQTKOPQ-----EDGQNNNL 396
DB 361 EFIFNREKLRQOGQSLLDTSRGGGQAQSKLQDGCNNNL 403

RESULT 8
US-10-254-869-5
; Sequence 5, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-5

Query Match 67.8%; Score 1425.5; DB 4; Length 403;
Best Local Similarity 68.2%; Pred. No. 4.1e-129;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGNANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDENEENVDHFDHFIILRAIGKSGFGKVCIVQKRDTKKMYAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFAAAMLPRETOITTM 180
DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFAAATVVKGAERASSM 180
QY 181 AGTKPYMAPEMES--SRKGAGYSPAVDWSLGVATAYELLRGRPPYHRSSTSSKEIVHTE 238
DB 181 AGTKPYMAPEVQVYMDRGPYSPVDWWSLGITAYELLRGRWPYEHSTVTPIDEILNMF 240
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQRFSDVQNSDQVFPYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSYTWCKGMVALLRKLTKDPESRVSSLDHDIQSVPYLADNMWDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKMRKCDSSQTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKRLAKNRSDGTCKDSCPLNGHLQHCLETVRE 360
QY 358 EFIFNREKVRNDFNKRQPNLALAEQTKOPQ-----EDGQNNNL 396
DB 361 EFIFNREKLRQOGQSLLDTSRGGGQAQSKLQDGCNNNL 403

RESULT 9
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/20996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match 62.9%; Score 1324; DB 4; Length 419;
Best Local Similarity 64.5%; Pred. No. 2.7e-119;
Matches 254; Conservative 53; Mismatches 77; Indels 10; Gaps 4;

QY 1 MGNANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMAMKYNKQKCV 60
DB 5 MSAATARR-PVFDKEDVNFDFHFIILRAIGKSGFGKVCIVQKRDTEKMYAMKYNKQKCI 63
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 64 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVQFSE 123
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFAAAMLPRETOITTM 180
DB 124 DTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFAAATVVKGAERASSM 183
QY 181 AGTKPYMAPEMES--SRKGAGYSPAVDWSLGVATAYELLRGRPPYHRSSTSSKEIVHTE 238
DB 184 AGTKPYMAPEIFHSGVNGGTGYSFVDMWSVGMAYELLRGRWPYDHSNAVESLVQLP 243
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQRFSDVQNSDQVFPYMDINWDVAFQKRLIPGF 298
DB 244 STVSQVYVPTWSEKEMVALLRKLTKVNPHEHLSLDVQVAPALAGVLDHLSKRVPEPGF 303
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQT--CLLQEHLDVQK 356

Db 304 VPKGRHLCHDPTFELEEMILESRLPHKKKRLAKNKSRLNDRSSQSENDYLDCLDAIQ 363
QY 357 KEPIIFNREKVNDRFNKQPNLALAEQTKDPQGED 390
Db 364 QDFVIFNREKL-----KRSQDLPREPLPAPESRD 392

RESULT 10
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-6

Query Match 62.6%; Score 1317.5; DB 4; Length 384;
Best Local Similarity 64.3%; Pred. No. 9.9e-119;
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;
QY 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCVNERVEV 65
Db 1 SARPPVDDKEDVNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCIERDEV 60
QY 66 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVFRELEILOEIEHVFVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVQFSEDTVRL 120
QY 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 185
Db 121 YICEMALALDYLRSHQIIHRDVKPDNILLDEQGHVHITDFNIAATIKDGERATALAGTKP 180
QY 186 YMAPEMFSS--RKGAGYSFAVDWWSLGVATAYELLRRRPHYHRSSTSSKBIVHTFTTVV 243
Db 181 YMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSSNAVESLVQLFSTVS 240
QY 244 TYPYSAWSQEMVSLKLLKLEPNPDQRFSLSDVQNFPPYNDINWDVAFQKRLIPGFIPNKG 303
Db 241 QYVPTWSKEMVALLRKLLTVNPEHRSFSLQDMQTAPSLAHVLDLSEKKVEPGFVPNKG 300
QY 304 RLNCDDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQT--CLLQEHLDVQKSEFII 361
Db 301 RLHCDPTFELEEMILESRLPHKKKRLAKNKSRLNDRSSQSENDYLDCLDAIQDFVI 360
QY 362 FNREKVNDRFNKQPNLALAEQTKDPQGED 390
Db 361 FNREKL-----KRSQELMSEPPPGPETS 384

RESULT 11
US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6

Query Match 62.6%; Score 1317.5; DB 4; Length 384;
Best Local Similarity 64.3%; Pred. No. 9.9e-119;
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;
QY 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCVNERVEV 65
Db 1 SARPPVDDKEDVNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCIERDEV 60
QY 66 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVFRELEILOEIEHVFVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVQFSEDTVRL 120
QY 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 185
Db 121 YICEMALALDYLRSHQIIHRDVKPDNILLDEQGHVHITDFNIAATIKDGERATALAGTKP 180
QY 186 YMAPEMFSS--RKGAGYSFAVDWWSLGVATAYELLRRRPHYHRSSTSSKBIVHTFTTVV 243
Db 181 YMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSSNAVESLVQLFSTVS 240
QY 244 TYPYSAWSQEMVSLKLLKLEPNPDQRFSLSDVQNFPPYNDINWDVAFQKRLIPGFIPNKG 303
Db 241 QYVPTWSKEMVALLRKLLTVNPEHRSFSLQDMQTAPSLAHVLDLSEKKVEPGFVPNKG 300
QY 304 RLNCDDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQT--CLLQEHLDVQKSEFII 361
Db 301 RLHCDPTFELEEMILESRLPHKKKRLAKNKSRLNDRSSQSENDYLDCLDAIQDFVI 360
QY 362 FNREKVNDRFNKQPNLALAEQTKDPQGED 390
Db 361 FNREKL-----KRSQELMSEPPPGPETS 384

RESULT 12
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match 60.8%; Score 1278.5; DB 4; Length 399;
Best Local Similarity 64.5%; Pred. No. 6e-115;
Matches 243; Conservative 52; Mismatches 73; Indels 9; Gaps 3;
QY 18 VNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCVNERVNVFKELQIMQ 77
Db 1 VNFDFEILRAIGKSGFGEVCIVQNDTKKCMKMYNKQKCIERDEVNVFRELEILOE 60
QY 78 LEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKLFCIELVMALDY 137
Db 61 IERVELVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVQFSEDTVRLYICEMALALDY 120

QY 138 QNQRIRHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTMAGTKPYMAPEMFSS--R 195
Db 121 RSQHIIHRDVKPDNILLDEQGHVHITDFNIAAMLPRETOITTMAGTKPYMAPEMFSS--R 180
QY 196 KGAGYSFAVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTPETTVVTPYPSAWQEMVS 255
Db 181 GGTGYSFEVDWWSLGTAYELLRGRPPYHRSSTSSKEIVHTPETTVVTPYPSAWQEMVS 240
QY 256 LKXKLLEPNPDQFSLQSDVQNPYMDINWDVAFQKRLIPGPIPNKGRNLCDPTFELEE 315
Db 241 LKXKLLEPNPDQFSLQSDVQNPYMDINWDVAFQKRLIPGPIPNKGRNLCDPTFELEE 300
QY 316 MILESPLHKKKRLAKKEDMKCDSSQT--CLLOEHLDSVQKEPIIFNREKVRDFTNK 373
Db 301 MILESPLHKKKRLAKKEDMKCDSSQT--CLLOEHLDSVQKEPIIFNREKVRDFTNK 355
QY 374 RQNLALQTKDPOGED 390
Db 356 RSQELMSEPPPPGPTSD 372

RESULT 13

US-09-841-683-7

; Sequence 7, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 236

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-7

Query Match 55.2%; Score 1161; DB 4; Length 236;

Best Local Similarity 90.2%; Pred. No. 6.1e-104;

Matches 222; Conservative 2; Mismatches 2; Indels 20; Gaps 1;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGCMKYMKNQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGCMKYMKNQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGTAYELLRGR 240
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGTAYELLRGR 220

QY 241 TVVTFP 246

Db 221 TVVTFP 226

RESULT 14

US-09-841-683-5

; Sequence 5, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 225

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-5

Query Match 55.0%; Score 1158; DB 4; Length 225;

Best Local Similarity 99.1%; Pred. No. 1.1e-103;

Matches 218; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGCMKYMKNQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKGCMKYMKNQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGTAYELLRGR 220
Db 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGTAYELLRGR 220

RESULT 15

US-09-819-607-2

; Sequence 2, Application US/09819607

; Patent No. 6686176

; GENERAL INFORMATION:

; APPLICANT: BEASLEY, Ellen et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001078

; CURRENT APPLICATION NUMBER: US/09/819,607

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 369

; TYPE: PRT

; ORGANISM: Human

US-09-819-607-2

Query Match 54.1%; Score 1137.5; DB 4; Length 369;

Best Local Similarity 62.8%; Pred. No. 2.1e-101;

Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;

QY 48 MCAMKYMKNQKCVNERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGD 107

Db 1 MYAMKYNKQOCIERDEVNVELEILQIEHVFLVNLWYSFQDEEDMFVVDLLGGD 60

Qy 108 LRYHLQONVHFKEETVKLFICELVMALDYLQONQRIIHRDMKPDNILLDEHGHVHTDFNI 167

Db 61 LRYHLQONVQFSEDIVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120

Qy 168 AAMLPRETOITTMAGTKPYNAPEMFSS--RKGAGYSFAVDWWSLGVATAYELLRGRPPYHI 225

Db 121 ATIIKGERATALAGTKPYNAPETIFHSFVNGGTGYSFEVDWWSVGMAYELLRGRPPYDI 180

Qy 226 RSSTSSKEIVHTFETTVVTPYPSAWSQEMVSLKKLLEPNPDQRFSQLSDVQNPFPYMNIN 285

Db 181 HSSNAVESLVQLFSTVSQYVPTWSKEMVALLRKLTVNPEHRLSSLQDVQAPALAGVL 240

Qy 286 WDAVEQKRLIPGFI PNKGRNLCDPTFELEEMILESPLHKKOKRLAKKMDMRKCDSSQT 345

Db 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESPLHKKOKRLAKKMRDNRDSSQS 300

Qy 346 --CLLQEHLDVQKEFIIFNREKVNRFNKRQPNLALQTKDPQGED 390

Db 301 ENDYLQDCLDAIQQDFVIFNREKL-----XRSQDLPREPLPAPESRD 342

Search completed: June 25, 2004, 10:51:42
Job time : 25 secs